

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 18:46:53 ; Search time 176 Seconds
 (without alignments) 5169.360 Million cell updates/sec

Title: US-09-975-842-1
 Perfect score: 404
 Sequence: 1 gggttggccgggttcaggat.....cccggtacttttagctctg 404
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Gaseq 101002: *

1: /SIDS2/gcdata/geneseq/geneseq/geneseqn-emb1/NA1980.DAT: *
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24: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	194.8	48.3	1743	Rose 1-aminocyclopentenyl
2	107.6	26.6	748	Arabidopsis thaliana
3	98.9	24.3	1384	Broccoli ACC synth
4	93.2	23.3	3438	DNA encoding a 1-a
5	86.6	21.4	961	1-aminocyclopropan
6	84.6	20.9	19	1-aminoacylcyclopropan
7	83.6	20.1	1170	ACC synthase GAC-2
8	83.6	20.1	18	Pelargonium 1-amin
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17	99.3	17	AAV30329	Pelargonium 1-amin

ALIGNMENTS

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FT	misc_feature	/note= "antisense oligonucleotide (Claim 18)" complement (251..300) /*tag= h	QY	185 TGTACGCTGCATTCGTTGGGGGTGAGAAACTCGGCATCGATGCAGGAGAGRC 244
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FT	misc_feature	/note= "any contiguous 50 nucleotides (Claim 18)" /*tag= n	QY	365 CTTGTGTCATGATGAGAACCAGGCTACTTAACTGCTCTAGGTAAGCTACTCCGGT 404
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XX	W09814465-A1.			
XX	09-APR-1998.			
XX	30-SEP-1997; 97WO-US17644.			
XX	01-OCT-1996; 96US-0724194.			
XX	(COIS) UNIV COLORADO STATE RES FOUND.			
PI	Ranu RS;			
XX	WPI; 1998-260994/23.			
DR	P-PSDB; AAW60239.			
XX	New isolated ACC synthase genes - are obtained from geranium and rose, used to develop products for producing plants with reduced ethylene levels, for increasing shelf-life			
PT	claim 6; Fig 9; 77PP; English.			
XX	CC 1-amino cyclopropane-1-carboxilate synthase (ACC synthase) (see AAW0239) of rose (cv. Red Cardinal). High quality mRNA was obtained from flower tissue using a novel adaptation of the 2-butoxyethanol precipitation technique. This was converted to cDNA and screened with a probe generated by PCR amplification (see AAV30328-29). The proseskcc7 clone was obtained. 3 Geranium ACC synthase clones (see AAV30324-26), are also claimed. The ACC synthase genes, or their fragments, when introduced in antisense orientation under control of a strong promoter, can be used to genetically modify a plant, especially geranium, rose or woody plant. As a consequence, the amount of ACC synthase produced in the plant cells is reduced and the rate of ACC conversion to ethylene decreases. This can be used to prolong the shelf-life of cut flowers and to reduce leaf yellowing and petal abscission during shipping and storage.			
CC	Sequence 1743 BP; 429 A; 401 C; 442 G; 471 T; 0 other;			
CC	Query Match 48 2%; Score 194 8; DB 19; Length 1743; Best Local Similarity 71 2%; Pred. No. 9 8e-58; Matches 285; Conservative 0; Mismatches 112; Indels 3; Gaps 2;			
CC	GTGGGGGTTCAGGATGGGGTTATCTACCTACGAGAACGAGCTACTCGCCA 64 1232 TTCCAGGTTCAGGGTGTGCGCATCTACAGAATGCTGACTGCGCTA 1291 65 AAAAGTTGAGGAGATTCACTACGAGGCTCCAGCAGCAGCGCTGCTGCTGTAAGC 124 1292 AAAGTGTGAGGTTCTCTCTATCTCCGCCCATCCACAGGGTGTGCTATGC 1351 1225 TCTGGGACAGGGTCACTCAAAGTTCATGAGGTAACAGAGGAACCTCAAAGAA 184			
XX	RESULT 2 ABQ65439/C ID ABQ65439 standard; DNA; 748 BP.			
XX	AC ABQ65439;			
XX	DE 21-AUG-2002 (first entry)			
XX	Arabidopsis thaliana polynucleotide SEQ ID NO 16.			
XX	KW Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease; stress; metabolic Pathway; biosynthetic pathway; nutrition; fungicide; insecticide; antibiotic; ds.			
XX	DR Arabidopsis thaliana.			
XX	OS OS			
XX	PN US2002059663-A1.			
PD	16-MAY-2002.			
XX	PR 26-JAN-2001; 2001US-0770149.			
XX	XX 27-JAN-2000; 2000US-178506P.			
PA	(GORBL/) GORLACH J.			
PA	(ANY/) AN Y.			
PA	(HAMI/) HAMILTON C M.			
PA	(PRIC/) PRICE J L.			
PA	(RAIN/) RAINES T M.			
PA	(YUYY/) YU Y.			
PA	(RAME/) RAMEKA J G.			
PA	(PAGE/) PAGE A.			
PA	(MATH/) MATHEW A V.			
PA	(LEDF/) LEDFORD B L.			
PA	(WOES/) WOESSNER J P.			
PA	(HAAS/) HAAS W D.			
PA	(GARC/) GARCIA C A.			
PA	(KRIC/) KRICKER M.			
PA	(SLAT/) SLATER T.			
PA	(DAVI/) DAVIS K R.			
PA	(ALLE/) ALLEN K.			
PA	(HOFF/) HOFFMAN N.			
PA	(HURB/) HURBAN P.			
XX	Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y, Haas WD, Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Hoffman N, Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N, Hurban P;			
XX	WPI; 2002-479224/51.			
XX	New nucleic acid that hybridizes to Arabidopsis thaliana sequences, useful e.g. for preparing transgenic plants with increased resistance or altered metabolism			

QY 301 AAGGAGAGCTGAGGCTATGGGACAACTTGCTAACTGCTAAGGAACTTGCTACTCC 360
 Db 1267 CAAGGCAGCTCGAGCTTGGATGTGATCTTGAAGAACTAAAGCTGAATATATCCT 1326
 QY 361 GGTTCTGTCATGATGACCCGGCTACTTACCTTGCTC 404
 Db 1327 GGATCTCGGCCATTGCTCGGAGTATGGATGTTAGGATTG 1370

RESULT 4
 AAX35671
 ID AAX35671 standard; DNA; 3438 BP.
 XX
 AC
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE DNA encoding a 1-aminocyclopropane-1-carboxylic acid oxidase.
 XX
 KW Localised mutation; target gene; plant cell;
 KW recombinogenic oligonucleobase; selective growth advantage;
 KW herbicide resistance; preservation; fruit; flower; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO9907855-A1.
 XX
 PD 18-FEB-1999.
 XX
 PR 05-AUG-1998; 98WO-US16267.
 XX
 PR 05-AUG-1997; 97US-0054836.
 XX
 PA (KIME-) KIMERAGEN INC.
 XX
 PI Arntzen CJ, Kipp RB, Kumar R, May GD;
 XX
 DR WPI; 1999-302251/25.

XX
 PT Introducing mutations into target genes in plant cells - using a recombinogenic oligonucleobase comprising 2 regions homologous to a target gene and an intervening mutant region
 PT XX
 PS Example 7; Page 46-47; 53pp; English.

XX
 CC The specification describes methods for introducing localized mutations into target genes in plant cells. The methods comprise using a recombinogenic oligonucleobase comprising 2 regions homologous to a target gene and an intervening mutant region. The methods can be used to introduce localized mutations into target genes to introduce desirable traits, e.g. selective growth advantage under appropriate selective conditions, change in colour of plant cells growing in a callus, herbicide resistance, or improved preservation of fruit or flowers. They can be used in plants such as maize, wheat, rice, lettuce, potato, tomato, canola, soybean or cotton cell. The present sequence represents a target for the methods of the invention.

XX
 SQ sequence 3438 BP; 1084 A; 647 C; 599 G; 1108 T; 0 other;
 Best Local Similarity 55.2%; Score 93.2; DB 20; Length 3438;
 Matches 223; Conservative 0; Mismatches 178; Indels 3; Gaps 2;

Query 1 GGGTGCCTGGGTTGAGATGGGTAACTACCTACACGGAAAGCTGCTACTACT 60
 Db 2294 GGCCTCCCTGGTTAGAGTTGGCCATTACTCCAAAGACAGATGTCATCTGCC 2353
 QY 61 GCCAAAAGTGTAGAGATTTCACTCCATTCACTCCACGCCGCGCTGCTGCTG 120
 Db 2354 GCTTCAAAATGTCAGTTGGCTTGCTGCTCCAGACACATACCTACTATCTCA 2413
 QY 121 ATGGCTCGGACAGCGGTTCACTCAAAGTCTCAGGTAACAGAGCGAACCTCAA 180

Db 2414 TTATTATCTGACAAGAAGTTCACTAAGAACACTACCTAGAGAGACCAAAACGGCTCAAG 2473
 QY 181 AGATGTAAGCTGCATCTGGGGGGTTGAGAAACTCGGCATCGATCGGAAAG 240
 Db 2474 AAGAGACAGAGAAAGCTGGTGGGCTAGGGCA-TCGGGATCAATGTCCTGAAAGAG 2532
 QY 241 CACCGGAGGCTCCTATGTTGGTCGACATGAGCGGATGATTCGATCCCTACAGGGAA 300
 Db 2533 TAATGCCGGG-ACTCTTTGTTGGTCGACATGAGCGGCTCCTAGATCTAACATCTCCT 2590
 QY 301 AAGGAGAGCTCAGCATGGGAACTTGCTAACATGCTAGGTAACAGGTTACTCC 360
 Db 2591 GAAGCGGAATGGATCTTGGAGAAGATGTTACGAGTGGAGCTAACATCTCCT 2650
 QY 361 GGTTCTGTCATGACCCGGCTACTTACCTTGCTC 404
 Db 2651 GGTCGCHGCGGCCATTGTTGAGAACCGGGTTGGTTAGAGTGG 2694

RESULT 5
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 ID AAV00220 standard; DNA; 961 BP.
 XX
 AC AAV00220;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE 1-aminocyclopropane-1-carboxylic acid synthase gene acacc3.
 XX
 KW 1-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple; flowering; inhibition; regulation; development; fruit; ss.
 XX
 OS Ananas comosus.
 XX
 Key FH Location/Qualifiers
 FT CDS 1..961
 FT /*tag= a
 FT /product= "acacc3"
 FT /*note= "no stop codon given; contains an intron"
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 FT /*tag= b
 FT /number= 1
 FT /*tag= c
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 FT /*tag= c
 FT 194..961
 FT /*tag= d
 FT /number= 2
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 PN AU9719963-A.
 XX
 PD 06-NOV-1997.
 XX
 PF 01-MAY-1997; 97AU-0019963.
 XX
 PR 01-MAY-1996; 96AU-0009582.
 XX
 PA (GOLD-) GOLDEN CIRCLE LTD.
 PA (QUEE-) STATE QUEENSLAND.
 PA (UYOO-) UNIV QUEENSLAND.
 XX
 PI Botella J, Sarnowski G;
 XX
 DR WPI; 1998-009229/02.
 DR P-PSB; AAW37445.
 XX
 PT New isolated ACC synthase genes from pineapples - used to generate transgenic pineapples in which the natural initiation of flowering is inhibited
 XX
 PS Claim 2; Fig 2; 37pp; English.
 XX
 CC The present sequence represents the nucleotide sequence encoding a

CC 1-aminoacyclopropane-1-carboxylic acid (ACC) synthase enzyme of
 CC pineapple. The present invention describes a transgenic variety of
 CC pineapple in which initiation of flowering is inhibited, the variety
 comprising a nucleotide sequence encoding an ACC synthase enzyme where
 the nucleotide sequence is operably linked, in the sense or antisense
 orientation, to one or more regulatory nucleotide sequences. The ACC
 synthase gene can be used to regulate pineapple plant development,
 particularly for inhibiting initiation of flowering. Such plants can
 then be induced to flower in a narrow spectrum of time which would
 thereby decrease the spread of fruit maturity within a crop.

Sequence 961 BP; 235 A; 246 C; 247 G; 233 T; 0 other;

Query Match 21.4%; Score 86 6; DB 19; Length 961;
 Best Local Similarity 55.9%; Pred. No. 9.2e-20; Indels 3; Gaps 2;
 Matches 205; Conservative 0; Mismatches 159; PS

1 GGGTGGCGGGGTCAGGATGGGGTTACTACTCTAACACAGGAAGAAGCTGTCACACT 60

QY 567 GGCGTACCGCCGCTTCGTCGGTGCAGTACCTCCAAATGGGGGGTCTCCACG 626

QY 61 GCGAAAGTGTGAGAGATTTCATCCATTCACTGCAGCTCGACCGAGCAGCTGGT 120

Db 627 GCGACCAAGATGTCGAGCTTGGGCTATCCTGACACTCAGTGTCTGTCCTG 686

QY 121 ATGCTCTGGACAGCGGTCACTCAAAGTTATCGAGGTAACAGAGCGAAACCAA 180

QY 687 TGTCTCTGCAGACAGGACTTCAGCAGCACTACATAGCGGAAACAAAGGGCT-TAG 745

QY 181 AGAAATGTCAGCTGATTGTGGGGGGTGTGAGAAACTCGGCATCGATGGACGGAA 240

Db 746 AGAGGGCAAAGGGCTCACCGAACGGCTGGGACATCGTATAACTGTTGGAG 805

QY 241 CAGGGAGCTCTATGTGGCCAGATGAGGGATTGATTCATCCATCAGCGAA 300

Db 806 CAAATGAGGT-TGTITGTGGTGGCATGAGGGACTTACTAAGCTTAAAGACCT 863

QY 301 AAAGAGAGCTGGACATGGGAACTTGTCAAGGAAACCTTACTCCC 360

Db 864 GAAGGAGKATGGAGCTGTGGAAAGATAGTCATGATGTGGGACTAACATTCTCG 923

QY 361 GTTCTT 367

Db 924 GGCTCTT 930

RESULT 6

AAV00219 ID AAV00219 standard; DNA; 968 BP.

XX AAV0219; AC

DT 08-JUN-1998 (first entry)

XX DE 1-aminoacyclopropane-1-carboxylic acid synthase gene acacc2.

XX 1-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple;

XX flowering; inhibition; regulation; development; fruit; ss.

OS Ananas comosus.

XX FH Key Location/Qualifiers
 FT CDS 1.:968
 FT /*tag= a
 FT /product= "acacc2"
 FT /transl_except= (pos:967..968 aa:Val)
 FT /note= "no stop codon given"

XX AUG979963-A. XX
 XX PD 06-NOV-1997. XX
 XX PF 01-MAY-1997; 97AU-0019953. XX

XX PR 01-MAY-1996; 96AU-0009582.

XX PA (GOLD-) GOLDEN CIRCLE LTD.

XX PA (QUEE-) STATE QUEENSLAND.

XX PA (YQD-) UNIV QUEENSLAND.

XX PI Botella J, Sanewski G;

XX DR WPI: 1998-009279/02.

DR P-PSDB; AAW37444.

XX PT New isolated ACC synthase genes from pineapples - used to generate
 PT transgenic pineapples in which the natural initiation of flowering
 PT is inhibited.

XX PS Claim 1; Fig 1; 37pp; English.

XX The present sequence represents the nucleotide sequence encoding a
 CC 1-aminoacyclopropane-1-carboxylic acid (ACC) synthase enzyme of
 CC pineapple. The present invention describes a transgenic variety of
 CC pineapple in which initiation of flowering is inhibited, the variety
 comprising a nucleotide sequence encoding an ACC synthase enzyme where
 the nucleotide sequence is operably linked, in the sense or antisense
 CC orientation, to one or more regulatory nucleotide sequences. The ACC
 synthase gene can be used to regulate pineapple plant development,
 particularly for inhibiting initiation of flowering. Such plants can
 then be induced to flower in a narrow spectrum of time which would
 thereby decrease the spread of fruit maturity within a crop.

XX Sequence 968 BP; 241 A; 235 C; 294 G; 198 T; 0 other;

Query Match 20.9%; Score 84 6; DB 19; Length 968;
 Best Local Similarity 52.7%; Pred. No. 4.7e-19; Indels 3; Gaps 1;
 Matches 208; Conservative 0; Mismatches 184; PS

1 GGGTGGGGGTCAGGATGGGGTTACTCTACACAGGAGCTGCTCAGT 60

QY 571 GGCTCCCGGTTAGGTGGGACGCTTACATCACATAGGGTGGACACG 630

QY 61 GCGAAAGTGTGAGGTTTACATCCATTGACTCGACAGGAGCTGGCTT 120

Db 631 GCGAGGAGATGTGAGGTTACACTGCTGCTCGAGACTAGAGGCTGGCTG 690

QY 121 ATGCTCTGGACAGCGGGTTACTCAAAAGTCATCGAGGAAACAGGAA 180

QY 691 ATGCTGCGACGAGGATCACAAGTACTACATAAGGACCAACAGGGAGGCTGAG 750

Db 181 AAGATGAGCTGTCATCTGGCGGGGTTGAGAAACTCGGCATCGATGGCAGGAAAG 240

QY 751 AGGGAGTACGAGTACATATCCAGGGGCTGAGAGCAGGGATGAGTCCTCCAGGG 810

QY 241 CACGGGGCTCTATGTGGCCGACATGAGGGATGATTGCGATCTACAGGAA 300

Db 811 AATGCCGGCTGTC---TGCTGGATGATCTGGGGCACTCTCGAGGAGAGAGA 867

QY 301 AAAGGAGCTGAGCATGAGGAACTGTGAAACATGTAAGGTAACACTTACTHCC 360

Db 868 GAAGGGAGCTGAGCTGTGGAACATGATTCATGAGGTTAGGCTCACATATCACC 927

QY 361 GGTCCTGTTGTCATTTAACCGGGCTCTT 395

Db 928 GGAATCTCATGCCACTGTCTGAGCCCTGGCTGGTT 962

XX RESULT 7
 XX ID AAT66247
 XX AC AAT66247;
 XX DT 28-JUL-1997 (first entry)

PT New isolated ACC synthase genes - are obtained from geranium and
 PT rose, used to develop products for producing plants with reduced
 PT ethylene levels, for increasing shelf-life
 XX
 PS Claim 1; Fig 5; 77pp; English.

CC This cDNA clone, designated pPHSacc49 (ATCC 98179), codes for a
 CC 55.1 kDa 1-laminocyclopropane-1-carboxylate synthase (ACC synthase)
 CC (see AAW6235) for geranium *x* hortorum cv. Sincerity).
 CC High quality mRNA was obtained from flower tissue using a novel
 CC adaptation of the 2-butoxyethanol precipitation technique. This
 CC was converted to cDNA and screened with a probe generated by PCR
 CC amplification (see AAV3028-29). The pPHSacc49 clone was obtained.
 CC Geranium ACC synthase cDNA clones pPHSacc41 (see AAV3034) and
 CC pPHSacc44 (see AAV3035), and rose ACC synthase cDNA clone pROSacc7
 CC (see AAV3030), are also claimed. These ACC synthase genes, or their
 CC fragments, when introduced in antisense orientation under control
 CC of a strong promoter, can be used to genetically modify a plant,
 CC especially geranium, rose or woody plant. As a consequence, the
 CC amount of ACC synthase produced in the plant cells is reduced and
 CC the rate of ACC conversion to ethylene decreases. This can be used
 CC to prolong the shelf-life of cut flowers and to reduce leaf
 XX yellowing and petal abscission during shipping and storage.

SO Sequence 1878 BP; 569 A; 390 C; 432 G; 487 T; 0 other;

Query Match 20.7%; Score 83.6; DB 19; Length 1878;
 Best Local Similarity 53.7%; Pred. No. 1.5e-18;
 Matches 217; Conservative 0; Mismatches 184; Indels 3; Gaps 2;
 QY 1 GGGTGGCCGGGGTGTAGGAGGGCCCTAATCTACTCTAACAGAGAACGGCTACTACT 60
 Db 953 GGCTTCTCTGGCTTAGGGTGGGATGTCATGAGCAGTGTGATGTT 1012
 QY 61 GCCAAAGTGTGACAGTTCATCCATTCAGCTGGCCCTGTTGACACAACTCACCCATGACCTGCTGCTCGTT 120
 Db 1013 GCGCCAAAGATGTCAAGTTCATCCATTCAGCTGGCCCTGTTGACACAACTCACCCATGACCTGCTGCTCGTT 1072
 QY 121 ATGCTCTGACACCGGGTCACTAAACTTCATCGAGGAAACAGAGGCGAAACTCAA 180
 Db 1073 ATGCTCTGACATGATGATCTGGACACATTCATCGTGGAGAGGGCGAGGGCTAGCC 1132
 QY 181 AGAGTACCTCTGCTTCTGGCGGAGAACCTGGCAGCCGGTGTGAGGAAACTTC 240
 Db 1133 AGAAGTGTACACACCTTCACAAAGAGGGCTGCA-CAGTGAACATGGATGCCAAAGAG 1191
 QY 241 CAGCGAGGGTTCTCTATGTTGGCCGACATGAGCGGATTGATGATCTGATCCTACAGCGGA 300
 Db 1192 CAATGGGGGTATTCAT--ATGGATGGCTTCAGAGGGCTTCAGAGAAACTTC 1249
 QY 301 AAAGGAGAGCTCGAGCTATGGAGAGTGTCTAACATGCTAAAGTAACTCCC 360
 Db 1250 GAGGGAGATGGCTGGAGAGGATTAATCAAGTGAAGCTAAATGCTGCCA 1509
 QY 361 GGTTCTGTTGTCATGTATGAGACCCGGTACATTAGCTCTG 404
 Db 1310 GGGGGCTGTCATGCTGGAGCCAGGGGGTTAGAGTGTG 1353

RESULT 9

AAT3139 ID Sequence 993 BP; 269 A; 233 C; 253 G; 238 T; 0 other;
 AAT3139 XX
 AC AAT3139; 3
 DT 07-DEC-1996 (first entry)

DE Broccoli ACC synthase cDNA clone TA13.

XX ACC synthase; 1-laminocycloproyl-1-carboxylic acid synthase;
 KW ethylene; shelf-life; Cucumis melo; melon; transgenic plant;
 KW antisense; broccoli; ss.

XX

OS Brassica oleracea.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 3..992
 FT primer_bind /*tag= a complement (1..14)
 FT /*tag= b /*note= "primer RMM494"
 FT primer_bind 975..993 /*tag= c /*note= "primer RMM491"
 FT /*note= "primer RMM491"
 XX
 PN WO9621027-A1.
 XX
 PD 11-JUL-1996.
 XX
 PR 07-JUN-1995; 95WO-US07271.
 XX
 PR 30-DEC-1994; 94US-0366932.
 PA (ASGR-) ASGROW SEED CO.
 XX
 PI Boesshore ML, Carney KJ, Deng RZ, Reynolds JF, Ruttencutter GE;
 XX
 DR WPI; 1996-334002/33.
 XX
 DR -PSDB; AAR98593.
 XX
 PT DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of
 PT Brassica oleracea - used to regulate ethylene-dependent processes
 PT in plants, esp. to improve shelf life
 XX
 PS Claim 3; Fig6a-C; 50pp; English.

CC Brassica oleracea cDNA clone TA13 (ATC33137) codes for
 CC 1-amino:cyclopropyl-1-carboxylic acid synthase (ACC-synthase)
 CC (AAR9599), an enzyme involved in ethylene biosynthesis. It was
 CC obtgd. by PCR amplification (see also AAV33140) of broccoli floret
 CC cDNA. The PCR product was cloned into pCR1 to obtain clone
 TA31. cDNA or genomic DNA (see also AAV3361) can be inserted, in
 CC sense or antisense orientation, into an expression cassette and then
 CC transferred to a binary vector suitable for Agrobacterium-mediated
 CC plant transformation. The constructs permit control of the level of
 ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis
 melo) and hence a control of maturation, ageing and shelf-life.
 XX
 SO Sequence 993 BP; 269 A; 233 C; 253 G; 238 T; 0 other;

Query Match 20.3%; Score 82.2; DB 17; Length 993;
 Best Local Similarity 55.0%; Pred. No. 3.3e-18;
 Matches 203; Conservative 0; Mismatches 163; Indels 3; Gaps 2;
 QY 1 GGGTGGCCGGGTCTGGAGGTTCTACTCTACAGCTGGCTACTACT 60
 Db 621 GGTCTTCTGGCTTCTGGAGGTTCTACTCTACAGCTGGCTACTACT 680
 QY 61 GCCAAAGTGTGACACGGGTCACTAAAGTCACTGAGGAAACTTC 120
 Db 681 GCGAGAAGGGATGTCGATTCACGCTGTCGCTCAGACACACAGTTGCTTCC 740
 QY 121 ATGCTCTGACACGGGTCACTAAAGTCACTGAGGAAACTTC 180
 Db 741 ATGTTGTCGGATGAGAGTGTACCGTGTAAAGGCTTGG 800
 QY 181 AGAATGTCACCTGCTTCGTCGAGGAGTGTACCGTGTAAAGGCTTGG 240
 Db 801 AGACGGTACAGACATGTTGAGGCTTAAAGGAGGTTGG 859
 QY 241 CAGCGAGGCTCTCTATGTTGGCCGACATGAGGGATTGATGCTGATCCTACGGAA 300
 Db 860 TAATGCGAGGT-TGTGCTGTTGGATGAATTTGGTTCTGTCGACAGGAACGAA 917
 QY 301 AAAGGAGAGCTCGAGCTATGGAGCACTGTTCTAACATWCTAACATWCTAACAGTGTAACTCCC 360

Db	918	CAAGGCAGCTCTGAGCTTGGGCTGATCTTGAAGAACATAAGCTGAAATATCTCCT	977
QY	361	GGTCTTGT	369
Db	978	GATCTTCGT	986
RESULT 10			
AAT73502			
ID			
AAT73502 standard; cDNA to mRNA; 1868 BP.			
AC			
AAT73502;			
XX			
DE			
DT			
XX			
DE			
Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS2.			
XX			
KW			
Ozone; induction; exposure; resistance; transgenic plant; ACC;			
1-aminocyclopropane-1-carboxylic acid biosynthesis; ds.			
OS			
Poplar nigra.			
XX			
FH			
Key			
Location/Qualifiers			
119..157 ⁹			
FT			
CDS			
/*tag= a			
FT			
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XX			
PN			
JP09075088-A.			
XX			
PR			
07-SEP-1995;			
95JP-0254510.			
XX			
PA			
(TOYT) TOYOTA JIDOSHA KK.			
XX			
DR			
WPI; 1997-239270/22.			
DR			
P-PSDB; AAW21755.			
XX			
PT			
Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic			
enzyme genes - from poplar tree, are useful for generating			
ozone-resistant trees and pollution clean-up trees			
XX			
PS			
Claim 2; Pages 9-11; 12pp; Japanese.			
XX			
CC			
This sequence, designated PNACCS2, is a 1-aminocyclopropane-1-			
carboxylic acid (ACC) synthase gene isolated from poplar trees which			
had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone			
for 6 hours after one hour acclimation at 25 degrees C, 70 % relative			
humidity, 30 k lux and air current 30 cm/second. This gene will be			
useful for breeding air pollutant ozone-resistant trees, especially			
poplar.			
XX			
SQ			
Sequence 1868 BP; 590 A; 366 C; 405 G; 507 T; 0 other;			
Query Match	20..3%	Score 82;	DB 18;
Best Local Similarity	53.5%	Length 1868;	
Matches	216;	Pred. No. 5.4e-18;	
Conservative	0;	Mismatches 185;	
Indels	3;	Gaps 2;	
QY	1	GGGTGGGGGTCTAGGATGGCGTATCTACTCTAACGAGAACGTGCTACT	60
Db	944	GGATCCCTCTGGCTCATGAGTGTACTCATACAGCTGAGTCGTTAATGTC	1003
QY	61	GCCAAAAGTGTACGAGATTCATCCATTCAGCTGGCTGAGCTGGCTTGCCTCGT	120
Db	1004	GGCCGAAGAGTGTCAAGTTGGCTCTCACAACTCAATTACTGCTCA	1063
QY	121	ATGCCTCTGACACGGGTCACTCAAAGTCATGAGAAACAGAGCAA	180
Db	1064	ATGCTTCTGATGAAGAGTGTGCGAGGATTCCTAGCCGAGACGTCGAAGGCTAAAG	1123
QY	181	AGAATGTAAGCTGTCATTCGGTGGGGGGTGAAGAACCTCGGACATCGGATGCA	240
RESULT 11			
AAT73501			
ID			
AAT73501 standard; cDNA to mRNA; 1864 BP.			
AC			
AAT73501;			
XX			
DE			
DT			
XX			
Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS1.			
XX			
KW			
Ozone; induction; exposure; resistance; transgenic plant; ACC;			
1-aminocyclopropane-1-carboxylic acid biosynthesis; ds.			
OS			
Poplar nigra.			
XX			
FH			
Key			
Location/Qualifiers			
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XX			
PN			
JP09075088-A.			
XX			
PD			
25-MAR-1997.			
XX			
PF			
07-SEP-1995;			
95JP-0254510.			
XX			
PR			
07-SEP-1995;			
95JP-0254510.			
XX			
PA			
(TOYT) TOYOTA JIDOSHA KK.			
XX			
DR			
P-PSDB; AAW21754.			
XX			
PT			
Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic			
enzyme genes - from poplar tree, are useful for generating			
ozone-resistant trees and pollution clean-up trees			
XX			
PS			
Claim 2; Pages 7-9; 12pp; Japanese.			
XX			
CC			
This sequence, designated PNACCS1, is a 1-aminocyclopropane-1-			
carboxylic acid (ACC) synthase gene isolated from poplar trees which			
had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone			
for 6 hours after one hour acclimation at 25 degrees C, 70 % relative			
humidity, 30 k lux and air current 30 cm/second. This gene will be			
useful for breeding air pollutant ozone-resistant trees, especially			
poplar.			
XX			
SQ			
Sequence 1864 BP; 574 A; 360 C; 392 G; 538 T; 0 other;			
Query Match	20..0%	Score 80..8;	DB 18;
Best Local Similarity	50.0%	Length 1864;	
Matches	202;	Conservative 0;	Mismatches 202;
Indels	0;	Gaps 0;	
QY	1	GGGTGGGGGTCTAGGATGGCTTACTCTACACGAGACGCTACT	60
Db	1025	GGCTTCCCTGGCTCAGGGTGGCTTACTCTACACGAGACGCTACT	1084

Query Match 19.5%; Score 78.8; DB 22; Length 1712;
 Best Local Similarity 53.0%; Pred. No. 6.9e-17;
 Matches 214; Conservative 0; Mismatches 187; Indels 3; Gaps 2;

Db 1045 GGGGGCGCAGGGCTTACGG-ACGGCCTCAAGGAGTCGGATTCAATGGACGG 1103
 QY 241 CAGGGAGGCTCTCTATGTCAGGGCCAGATGAGCGGGATGATTCGAATCCTACAGCAA 300
 CC 1104 CAAGCGGG- -GTGTCGCTGGATGGACTTGAGGGCTTGCTGAAGGGACGG 1161
 QY 301 AAAGGAGCTCGAGCTATGGACAAAGTGTCAAACATGCTAAGTAAACCTACTCCC 360
 Db 1162 GAGCGGGAGCTCCGGCTGTCGCGGGTGAATCATCACAGCGTGAAGCTCACATCTCGCC 1221
 QY 361 GGTCTCTGTGATGTAATGAGCTGGACCCGGCTACTTTAGCCTCTG 404
 Db 1222 GGGCGCTTCCACTGCTGGAGCCGGGGTGGTCAAGGGTG 1265

RESULT 15

AAS9901
 ID AAS9901 standard; cDNA: 1712 BP.
 XX
 AC AAS9901;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE DNA encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS).
 XX 1-aminocyclopropane-1-carboxylic acid synthase; ACS; banana;
 KW ethylene biosynthesis; ethylene-forming enzyme; EFE; fruit ripening;
 XX fruit storage; ss.
 OS Musa sp.
 XX
 PN US6262346-B1.
 XX
 PD 17-JUL-2001.
 XX
 PP 15-JAN-1999; 99US-0231240.
 PR 15-APR-1996; 96US-0632598.
 PA (ZENE) ZENECA LTD.
 XX
 PI Bird CR, Fletcher JD;
 XX
 DR WPI; 2001-450497/48.

PT Modifying level of ethylene biosynthesis in plant of genus Musa, involves inserting into genome of plant a DNA sequence encoding, banana 1-aminocyclopropane-1-carboxylic acid synthase or ethylene-forming enzyme -

XX
 PS
 XX
 XX
 CC The sequence represents the coding sequence of 1-aminocyclopropane-1- carboxylic acid synthase (ACS) from banana, used in the method of
 CC the invention. The method involves modifying the level of ethylene
 CC biosynthesis in a plant of the genus Musa by inserting into the genome of
 CC the plant a DNA sequence (1) encoding a banana 1-aminocyclopropane-1-
 CC carboxylic acid synthase (ACS) or an ethylene-forming enzyme (EFE), where
 CC (1) is in sense or antisense configuration, and modifies the level of
 CC activity of ACS or EFE, thus retards the rate of ripening in banana
 CC fruits which reduces the rate of deterioration of banana fruit after
 CC harvest. As a result, fruit may be harvested when they have reached
 CC partial or full ripeness and still have the robustness to withstand
 CC handling and transport to reach the consumer in good condition. In this
 CC way high quality ripe fruit can be made available to the consumer with
 CC reduced requirement for post-harvest treatment. High quality fruit will
 CC have improved flavour and texture. High quality fruit can be produced
 CC consistently over a wide harvest period, and such fruit can be held in
 CC store for long periods and ripened to optimal quality by the supply of
 CC exogenous ethylene.

XX Sequence 1712 BP; 397 A; 459 C; 478 G; 378 T; 0 other;

Query Match 19.5%; Score 78.8; DB 22; Length 1712;
 Best Local Similarity 53.0%; Pred. No. 6.9e-17;
 Matches 214; Conservative 0; Mismatches 187; Indels 3; Gaps 2;

Db 865 GGCCTCCCTGGCTCCGCCCTGGGTCTATACTCCTACAGCTAACACGAGAACGGCTACT 60
 QY 61 GCGAAAAGTGTGAGGAGATTTATCCATTCTAGCTCGAGCGAGGGTTGCCGCTCTT 120
 Db 925 GCGAGGAATATGAGCTTGAGCTTGACTGTTGCTGTCGAGCAGCAGCTCGCTGCTT 984
 QY 121 ATGCTCTGGACACGGGTTACTCAAAGTCATCGAGGTAACAGGGAAACTCAA 180
 Db 985 ATGTTGGAGACGGAGAGTTACCCAGAGTTCTAGGAGCTGAGCTGTCG 1044
 QY 181 AGAATGTAACGCTGCAATTCTGGGGGGTGTGAGAAACAGTGGCATCCGATGACAGGAAG 240
 Db 1045 GGGCGCCGAGGGCTTACGG-ACGGCCTCAAGGAGTCGGATTCAATGCTGGACGG 1103
 QY 241 CAGGGAGGCTCTCTATGTCAGGGCCAGATGAGCGGGATGATTCGAATCCTACAGCAA 300
 Db 1162 GAGCGGGAGCTCCGGCTGTCGCGGGTGAATCATCACAGCGTGAAGCTCACATCTCGCC 1221
 QY 361 GGTCTCTGTGTCATGTTATGACCCGCTACTTTAGCCTCTG 404
 Db 1222 GGGCGCTTCCACTGCTGGAGCCGGGGTGGTCAAGGGTG 1265

Search completed: March 11, 2003, 00:52:07
 Job time : 181 secs



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OM nucleic - nucleic search, using sw model

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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(without alignments)
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Searched:

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Maximum Match 100%

Listing first 45 summaries

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8: qb_pl:*

9: qb_pr:*

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11: qb_sts:*

12: qb_sy:*

13: qb_un:*

14: qb_v1:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_lnu:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_v1:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_man:*

37: em_htg_irr:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Result No. Score % Query Match Length DB ID Description

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3	147.8	36.6	1674	8	AF348575	AF348575 Arabidops	
4	147.8	36.6	1757	8	AY054691	AY054691 Arabidops	
5	147.8	36.6	98412	8	FL16P1	AC011000 Sequence	
6	146.8	36.3	1089	8	TAU3779	U35779 Triticum ae	
7	144.2	35.7	143113	8	AF00559	AF00559 Oryza sat	
8	127.6	31.6	1488	8	AF336920	AF336920 Arabidops	
9	127.6	31.6	86212	8	AB010074	AB010074 Arabidops	
10	117.2	29.0	1372	8	MSBACSYN	X95947 Musa acuminata	
11	114	28.2	1812	8	MSBACSYN	X95946 Musa acuminata	
12	110.8	27.4	1400	8	AF312737	AF312737 Malus x d	
13	110.8	27.0	8	MSU03294	U03294 Malus sylve		
14	110.8	27.4	1633	8	MD0011518	AJ0011518 Malus dom	
15	110.8	27.4	1778	8	AB015624	AB015624 Pyrus pyr	
16	110.8	27.4	1812	8	PCPACSYN	X87112 P. communis	
17	110.8	27.4	2004	8	MAUACSYN	LM3347 Malus domes	
18	110.8	27.4	5526	8	MD189156	U89156 Malus domes	
19	109.2	27.0	4405	8	AF151961	AF151961 Vigna rad	
20	109.2	27.0	8	AF334720	AF334720 Arabidops		
21	107.6	26.6	1344	8	ATTHAC55B	AJ32390 Arabidops	
22	107.6	26.6	5676	8	AB010102	AB010102 Malus dom	
23	107.6	26.6	89904	8	AT25K17	AB049171 Arabidops	
24	107.6	26.6	196286	8	ATCIRIV64	AL161564 Arabidops	
25	106	27.0	3758	8	VRU34987	U34987 Vigna radia	
26	104.8	25.9	1413	8	AF049711	AF049711 Petunia x	
27	104.8	25.9	1413	8	AB018355	AB018355 Vigna rad	
28	104.8	25.9	1873	8	AB000679	AB000679 Vigna rad	
29	104.8	25.9	1892	8	VRU34955	U34986 Vigna radia	
30	104.8	25.9	3234	8	NTA131837	AJ131837 Nicotiana	
31	104.8	25.9	4284	8	ATRAC55B	L29260 Arabidopsis	
32	104.8	25.9	4714	8	AB018355	AB018355 Vigna rad	
33	104.8	25.9	84440	8	AB010075	AB010075 Arabidops	
34	104.8	25.9	118086	8	ATP16H1	AJ021684 Arabidops	
35	103	25.5	1089	8	AB021908	AB021908 Musa acuminata	
36	102.8	25.4	1410	8	AF334712	AF334712 Arabidops	
37	102.8	25.4	1413	8	AF332391	AF332391 Arabidops	
38	102.8	25.4	1638	8	CUCACCA	DO103 Cucurbita m	
39	102.8	25.4	4346	8	CMW3774	U3774 Cucurbita m	
40	102.8	25.4	4711	8	ATP16K5	AL132665 Arabidops	
41	102.8	25.5	10766	8	ATP28119	AL03509 Arabidops	
42	102.8	25.4	19893	8	ATCHRIV8	AL161592 Arabidops	
43	101.2	25.0	1115	8	AF338651	AF338651 Brassica	
44	101.2	25.0	1393	8	M94863	M94863 Vigna radia	
45	101.2	25.0	1393	8	VRACCSYNT	212134 V. radiata g	

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

ORGANISM
Prunus armeniaca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicots; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE
1 (bases 1 to 894)
Mbouie-A-Mbouie,D. and Fils-Lycaon,B. R.

AUTHORS
TITLE
Molecular cloning and nucleotide sequence of genomic DNA encoding

FEATURES	source	AC ^C synthase from apricot fruit
REFERENCE	Unpublished	
AUTHORS	2 (bases 1 to 894)	
TITLE	Mbeguie-A-Mbague,D. and Fils-Lycaon,B. R.	
JOURNAL	Submitted (07-SEP-1999) Station de Technologie des Produits	
VEGETAUX, Institut National de la Recherche Agronomique, Agroparc-Domaine Saint Paul, Avignon 84914, France	Location/Qualifiers	
FEATURES	source	1. .894
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	/ab_xref="Taxon:36596"	
gene	<1. .>894	
mRNA	/gene="ACSL1"	
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CDS	/product="AC ^C synthase"	
	/protein_id="PAGI6977.1"	
	/ab_xref="GI:1041265"	
	/note="PA-ACSL1"	
	/codon_start=1	
	/product="AC ^C synthase"	
	/protein_id="PAGI6977.1"	
BASE COUNT	250	a 177 c 204 g 263 t
ORIGIN		
Query Match	48.6%	Score 195.4; DB 8; Length 894;
Best Local Similarity	71.5%	Pred. No. 1.2e-51; Mismatches 111; Indels 3; Gaps 2;
Matches	286;	Conservative 0; Mismatches 111; Indels 3; Gaps 2;
Db	5	TGCCGGGTTCAGGTGGCGTTACTCTCTAACAGAGAACGTGCTCACTTGCC 64
Qy	497	TTCCAGGTTAGGGGGGTATCTACTCCATCCATGGTGTCTGCTGCTGCTGCTA 556
Db	65	AAAGGTGAGGAGTTTCATCCATTAGCTGGACGAGCGCTGCTGCTGCTGCTA 124
Qy	557	AAAGTTAACAGGTTCTGTCCTTCACTCCATCCAAAGCTGTTCTATAGTC 616
Db	125	TCTGGACAGCGCGTTACTCAAAAGTCATCGGGTAAACAGAGCGAACTCAAAAGA 184
Db	617	TTCAGACACCAAAATTGTCCAAAGTTATGTAGGCCATAGAGAGACTTGAGGA 676
Qy	185	TGTTCGTCGATGTTGGGGGTTGAGAAGACTCGCATCCGATGCGGAAAGCGC 244
Db	677	TGACCTTAATCTGAC-AGGGTGAACATTGGGATGTGTACAAAGGCAAT 735
Db	245	GGAGCTCTCTATGTGGGCCACATGAGCGATTGATTGATCTACAGGGAAAG 304
Qy	736	GGAGG-TTTCAGGTGGCACATGAGTGGTTAATCCGCTCTTACAAAGAGAAG 793
Qy	305	GAGGCTCGAGCTAGGACAGTGTCAAATGCTAGGTAACGTACTCCGGTT 364
Db	794	GGGAGCTGAGCTGGGATAGGTGTGAGCTAGGTAATGTAACCTCCGGAT 853
Qy	365	CTTGTGTGATGGTGAACCCGCTACTTTAACCTCTG 404
Db	854	CTTCAGTCATGTATTGAAACCCGCTGGTCCCGCTCIG 893
RESULT 2		
AF116028	AF146028	581 bp DNA linear PLN 17-MAY-1999
DEFINITION	Actinidia chinensis 1-aminocyclopropane-1-carboxylate synthase 3	
ACCESSION	Gene, Partial cds.	
VERSION	AF146028.1	GI:4836802
KEYWORDS		
FEATURES	source	Actinidia chinensis.
REFERENCE	Unpublished	
AUTHORS	1 (bases 1 to 581)	
TITLE	Xu,C., Chen,K., Chen,D. and Zhang,S.	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 581)	
AUTHORS	Xu,C., Chen,D., Chen,K. and Zhang,S.	
TITLE	Direct Submission	
JOURNAL	Submitted (27-APR-1999) Department of Horticulture, Huaijachi Campus, Zhejiang University, Kaixuenu 268, Hangzhou, Zhejiang 310029, People's Republic of China	
FEATURES	source	Location/Qualifiers
	/organism="Actinidia chinensis"	
	/ab_xref="Taxon:3623"	
	/note="Actinidia chinensis	
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	/codon_start=3	
	/product="1-aminoacyclopropane-1-carboxylate synthase 3"	
	/protein_id="PADD30563.1"	
	/ab_xref="GI:4836802"	
	/note="ACSL3"	
	/codon_start=3	
	/product="1-aminoacyclopropane-1-carboxylate synthase 3"	
	/protein_id="PADD30563.1"	
BASE COUNT	166	a 112 c 132 g 171 t
ORIGIN		
Query Match	44.1%	Score 178; DB 8; Length 581;
Best Local Similarity	70.3%	Pred. No. 9e-46; Mismatches 110; Indels 3; Gaps 2;
Matches	267;	Conservative 0; Mismatches 110; Indels 3; Gaps 2;
Db	10	GGGTTCAGGATGGGGTTACTACTCTCAACAGAACGTGCTCACTACTGCCAAAG 69
Qy	204	GGTTTCGGATGGGGTTACTACTCTCACTTCAGTGGAAATGCTGCTGCTGCTG 263
Db	70	TGGAGGAGTTTCACTCCATGCGCTGGAGCGCTGCTGCTGCTGCTGCTG 129
Qy	264	CTAACAGATTCGCACTTTCAGCTCCACCCAACTGCTCTATCCTAACATGCTTCT 323
Db	130	GACACGGGTTTCACTCAAAGTTCATCGAGGTAACAGAGGAAACTCAAAGATGAC 189
Qy	324	GATACAATTTCGCGATAGTTTACAGACACATCGGAAAGGCTCCACGGATTG 383
Db	190	GCTGCAATTGGGGGTTGAGAAGACTCGCATCCGATGCGGAAAGCGACGGGAG 249
Qy	384	AGTGGATTCGTTGGGATGAAAGCGATTAGGTATAGATGGCCTAAAGCAATGCGG 442
Db	250	CTTCATATGTTGGCCACATGCGGATTGATGCTACAGGAAAGGAGG 309
Qy	443	-TTCTATGTTGGCTGATCGCTGGTGTGATCTGCTCATAGCTGAGAAAGGGAG 500
Db	310	CTCGAGCTAGGGACAGTGTCAAATGCTAGGTAACGTACTCCGGTCTGT 369
Qy	501	CGAACGCTGGGATAGTTGATGACTGCTAGGTATGTAACCTCTGGATCTCC 560
Db	370	TGTCATTGTTGAAACCCG 389
Qy	561	TGTCAGTGTATTGAAACCTG 580
RESULT 3		
AF34575	AF348575	1674 bp mRNA linear PLN 18-APR-2002
DEFINITION	Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate synthase	
ACCESSION	AC510 (At1g62960) mRNA, complete cds.	
VERSION	AF348575	
KEYWORDS		

VERSION	Db
AF348575.1	GI:133194767
KEYWORDS	FLL-CDNA.
SOURCE	Arabidopsis thaliana.
ORGANISM	Arabidopsis thaliana.
REFERENCE	1 (bases 1 to 1674)
AUTHORS	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Cheuk, R., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Davis, R.W., Ecker, J.R. and Theologis, A.
TITLE	Direct Submission
JOURNAL	Submitted (13-FEB-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
FEATURES	Location/Qualifiers
source	1 .1674 organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" /clone="C00005" /note="This clone is in pUNI-T3-D/V5-HIS-TOPO. ecotype: Columbia" 1. .1674 /gene="At1g62960" 1. .1674 /gene="At1g62960" /codon_start=1 /evidence=experimental /product="1-aminocyclopropane-1-carboxylate synthase AC510" /protein_id="AAK151546.1" /db_xref="GI:133194768", /transliteration="MTREPNRSNSNSDKNSCNVGGGTTGMRVIVP1QGVWQGR GCFGLGSPVCPAFYFQFQYFLKRRKNDKIDSNSGNSNSASSSSNSGNSLDPTRSG AGHLTELGPLPRLSRNLKLSLSPRNSGVLQAVSUSGRVNLKGGDSSPPVQKRVEDDE DELGNGPDCYIQGLQANQLNLSDLWNLKEA1SDGLTSIGTASPEPDSLDELLKMA VAGFMTETAKNSVIFPDSOLVITSGASSATEISLSCLDGNSAFLVPTPESPGYDVK KNFTGVIDLHVPOKSDASNSMMSVFLDRAFTYQAKKRGVRKGTSNPSNEMGSLJRS ENYUALLPARERNHILNEIRAGSVHREGEVHPSMELTDVENDRERVHIVD SKDLSFRCJRSAAYSFNSBVSLSRKLTFLSPVSPSTQHLLTASINPKVWRFKT NRQLQSIITELVEGLKPLWKGRLIECFTSRNSGGFICWADMRRGLISSSEKGEILWNKLNI GKINVNPSCCHCPLWKGRLIECFTSRNSGGFICWADMRRGLISSSEKGEILWNKLNI
BASE COUNT	443 a 343 c 403 g 485 t
ORIGIN	Query Match 36 5%; Score 147.8; DB 8; Length 1674; Best Local Similarity 63.3%; Pred. No. 5.2e-36; Matches 256; Conservative 0; Mismatches 142; Indels 3; Gaps 2;
Qy	4 TTGGCGGGGCTCAGATGGCGCTAATCTACTCTCTACGAGACGTGCTACTAGGCC 63
Db	1192 TTGGGGGGCTCAGATGGCGCTAATCTACTCTACGAGACGTGCTACTAGGCC 1251
Qy	64 AAAAGTGTAGCAGGATTTATCCATTCTAGCTCGACGAGCGCTTGCTCTCGTTATG 123
Db	1252 AGAAAGCTCAGGCGCTCAGCTCTACCTGTCTCATCTCCACACATTGTGATATCCGA 1311
Qy	124 CTCTGGAGACGCGGTTCAACTAAAGTCTACGAGGTAACAGACGGAAACTCAAAGA 183
Db	1312 ATCTCCAACTAAAGATGTCAGAGATTGTGAAACACAGGCGAGATGTGCAAGT 1371
Qy	184 ATGTAAGCTGCAATGTTGCGGGGTTGAAACACTGGCATCCGATCGCACGAAAGCAG 243
REFERENCE	2 (bases 1 to 1674)
AUTHORS	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etgu, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
TITLE	Arabidopsis Open Reading Frame (ORF) Clones
JOURNAL	Unpublished
FEATURES	Location/Qualifiers
source	1 .1674 organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" /clone="C00005" /note="This clone is in pUNI-T3-D/V5-HIS-TOPO. ecotype: Columbia" 1. .1674 /gene="At1g62960" 1. .1674 /codon_start=1 /evidence=experimental /product="1-aminocyclopropane-1-carboxylate synthase AC510" /protein_id="AAK151546.1" /db_xref="GI:133194768", /transliteration="MTREPNRSNSNSDKNSCNVGGGTTGMRVIVP1QGVWQGR GCFGLGSPVCPAFYFQFQYFLKRRKNDKIDSNSGNSNSASSSSNSGNSLDPTRSG AGHLTELGPLPRLSRNLKLSLSPRNSGVLQAVSUSGRVNLKGGDSSPPVQKRVEDDE DELGNGPDCYIQGLQANQLNLSDLWNLKEA1SDGLTSIGTASPEPDSLDELLKMA VAGFMTETAKNSVIFPDSOLVITSGASSATEISLSCLDGNSAFLVPTPESPGYDVK KNFTGVIDLHVPOKSDASNSMMSVFLDRAFTYQAKKRGVRKGTSNPSNEMGSLJRS ENYUALLPARERNHILNEIRAGSVHREGEVHPSMELTDVENDRERVHIVD SKDLSFRCJRSAAYSFNSBVSLSRKLTFLSPVSPSTQHLLTASINPKVWRFKT NRQLQSIITELVEGLKPLWKGRLIECFTSRNSGGFICWADMRRGLISSSEKGEILWNKLNI GKINVNPSCCHCPLWKGRLIECFTSRNSGGFICWADMRRGLISSSEKGEILWNKLNI
COMMENT	e-mail for correspondence: arab@sequence.stanford.edu
TITLE	Direct Submission
JOURNAL	Submitted (28-AUG-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
FEATURES	Location/Qualifiers
source	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RFLP cDNAs (RAFL cDNA), "RIKEN Arabidopsis Full-Length cDNA": Seki, M., Narusaka, M., Ishida, J., Satoh, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
Qy	The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
Db	Southwick, A. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.
FEATURES	Location/Qualifiers
source	1 .1757 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" /clone="RAFF04-20-B08" /note="This clone is in pBluescript" 1 .1757 /gene="At1g62960; F16p17.11" 39. .1712 /gene="At1g62960; F16p17.11" /codon_start=1 /product="Strong similarity to AC55 from Lupinus albus domain PF00155"

LLAMANGEDDVLDVLIDTSSV" gene
 18492. .19560
 /gene="F16P17_3"
 join(18492. .18563, 19155. .19336, 19434. .19560)
 /gene="F16P17_3"
 /note="Contains similarity to a 14kDa protein found on
 ER-derived vesicles from *Saccharomyces cerevisiae*
 gi|621384. ESTS gb|T22150, gb|A1100633, gb|AA395672 come
 from this gene."
 /codon_start=1
 /evidence="not_experimental"
 /protein_id="AAF75818.1"
 /db_xref="GI:8493595"
 /translation="MGEVWWTWISLFLITLTLGLIVQLISLADLEFDYINPYLSASR
 INFVWLPESILOGFCVYVLTGHWEMALCVPVLYNFHLSRKOHLDIVTEIFNL
 DWKEKKRLEKLAUYLTILTLTIFIN"
 misc_feature
 CDS
 gene
 /note="Contains similarity to Limpetl_transposon."
 /codon_start=1
 /evidence="not_experimental"
 /protein_id="AAF75800.1"
 /db_xref="GI:8493577"
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 IWMKILHEMTDOKVILKKNWISLPEKGVVLTVEVVEPEEPKINDISSNIVGMD
 IMLAVSSGGERSISQFETLASDSDGFLRCBIICHAFSYSVIELK"
 gene
 /note="F16P17_4"
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 CDS
 gene
 /note="Contains a RepB PF|01051 protein domain and
 multiple PPR PF|01535 repeats."
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 /protein_id="AAF75801.1"
 /db_xref="GI:493578"
 /translation="MORSTLSTARLFLVHNLOQIGNPNTVPSFNLGGCWRSA
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 NGYHHSKRISDAVALDQWEMVKGKDPITFTTILHGELHNKASEVALDQVQRG
 CQPDIVTYGIVNNGLICKRGKGIDIALSLSLRKMEKRLEADWVYNTIDGLCKRHMDD
 ALNLTETMDNGTRDVFYVSSLSLSCNGWADASRLSDMWERKINPVVNTFSA
 DCFFPANVVIITSLKGCKAKRVEGSMELPREMSORGVLGVMTVTTLHGFFQRDCD
 NAQWFKQWMSVGHNPNTYNTIDGLICKRGKGKAKAMVYFEYVYRSTEPMPTYNT
 MTECMACKVEDWELFNLUSQPKVSPNVIAYVMTSFCRKSKRSEADSLKRMKME
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 27943. .29529
 gene
 /note="F16P17_5"
 27943. .29529
 CDS
 gene
 /note="Contains a RepB PF|01051 protein domain and
 multiple PPR PF|01053 repeats. EST gb|AA728420 comes from
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 /evidence="not_experimental"
 /protein_id="AAF75802.1"
 /db_xref="GI:8493579"
 /translation="MLAKTSSARFVRHSLVVGNAATPLSSFCRRAFSGKTSY
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 KMETLGISHLNTTINLINCFCRSLSLALAGKMKMGYEDIVTNSLNGFCH
 GNRSDAVALDQWEMGKRPDTWFTTLLHGILHNSKASEVALDQVQGDPL
 VTYAUVNGLICKRDTDLALNHLNMAKTEAUNVHTKNSVYDLSICKYRDRDQPL
 TEMENKGIVPNTYTTSLTSCLCNGWISDASRLSDMTERKINPVLFSALIDAFV
 KKGKLVKAERLYEMIKRSIDPNTFVSSLINGFCMDRLGEARQMLEMIRKDCLPN

RESULT 6
 TAU35779 LOCUS TAU35779 1089 bp mRNA linear PLN 07-NOV-1996
 DEFINITION Triticum aestivum 1-aminocyclopropane-1-carboxylate synthase (ACSL)
 mRNA, partial cds.
 ACCESSION U35779
 VERSION U35779.1 GI:1173637
 KEYWORDS

SOURCE	Triticum aestivum.
ORGANISM	Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
REFERENCE	1. (bases 1 to 1089) Subramanian, K., Abbo, S. and Deng, P.P. Isolation of two differentially expressed wheat ACC synthase cDNAs and the characterization of one of their genes with root-predominant expression
AUTHORS	Subramanian, K.
TITLE	Plant Mol. Biol. 31 (5), 1009-1020 (1996)
JOURNAL	Plant Mol. Biol. 31 (5), 1009-1020 (1996)
MEDLINE	97000913
PUBMED	8843943
REFERENCE	2. (bases 1 to 1089) Subramanian, K.
AUTHORS	Subramanian, K.
TITLE	Direct Submission
JOURNAL	Submitted (11-SEP-1995) Kuppuswamy Subramanian, USDA-ARS, Beltsville Agricultural Research Center, Plant Molecular Biology Laboratory, Beltsville, MD 20705, USA
FEATURES	Location/Qualifiers
SOURCE	1. .1089 /organism="Triticum aestivum" /clone="PwAS-1" /db_xref="taxon:4565" /EC_number="4.4.1.14" /note="ACC synthase" /codon_start=1 /product="1-aminocyclopropane-1-carboxylate synthase" /protein_id="PAB1418_1" /db_xref="GI:1173638" /translation="MGLABNHLSDLVREMMERHAGPANTPAGDEERDTLSGLATYQPGDITAKMAGFMRMORIMHSVSEPSOMWITSGATPAMEILSSCADPNAFLYPSPIYFGWDRDKWRTGELIPCRSTDNFNISITALEIYQAKKRGVRYVGVLISNPSPMTGSEPVPKDPLDUDLFRATVKNHLSIDSEFAGSDFGSEEFVSAEVNLEDFDRRHYIYGLSKDLSLAGFVYIISNEEAAKARFESVSTSTQRLVAVMLSDQKTSNLYKVNRLRKAAYNLYDQKVGICBCKFSSGGFYCWADMFSKIRSYSEKGERTLDRILKEAKNTVPESSCHIEPGW"
BASE COUNT	274 a 248 c 303 g 264 t
ORIGIN	
Query Match	36.3%; Score 146.8; DB 8; Length 1089;
Best Local Similarity	64.8%; Pred. No. 1e-35;
Matches	249; Conservative 0; Mismatches 132; Indels 3; Gaps 2;
QY	8 CGGGGTTAGGATGGGGTATCCTACTCCPACACAGAGACGTCGCTACTCCAAA 67
Db	707 CAGGGTTGAGTCAGTCAGGATCATGATTCGTTAAAGAACGATTGAGGCC 766
QY	68 AGTTGACGAGATTTCATCCATTGCTGCTCCGAGCAGCGCTTGCTGCTATGCTC 127
Db	767 AGATGCCAGATTCTCATCGTGACGCCAGGCCAGGCCCTTGTGCAAGCTT 826
QY	128 CGGACAGCGCGTTCAAAAGTCATCAGGTTAACAGAGCGAACTCAAGAATGT 187
Db	827 CGGACCCAGAAGTTTATTCGAAATTACCTGAGAGAGGGCTGGCAAGGCT 885
QY	188 ACGCGCATCGTGGCGGGGTTGAGAAACTCGCATCGATCGCAAGGAGCGGA 247
Db	887 ACAATCTGCTGCTGAT-ATGCTTGTGAGCAGGTGCGATCGTCTCAAGAGCGGA 945
QY	248 GGCTCTCATTTGTTGGCGGACATGAGCGATGATTCGATCCAGGAAAGGG 307
Db	946 GGTT--TCTACTCGTGGCGAGACAGCAGTCATCCGGTCTTACAGCGAGAAAGGAG 1003
QY	308 AGCTGAGCTATGGCAAGTGTAAACATGCTAAGGTAACAGCTACTCCGGTCTT 367
Db	1004 AGCGGAGGCTTGGCACAGGTGTTGGAGGGCGAGGCTAACGTCACCCAGSTCAT 1063
QY	368 GTTGTGTCATTGTTGAAACCCGGCT 391
FEATURES	Location/Qualifiers
SOURCE	1. .143113 /organism="Oryza sativa (japonica cultivar-group)" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="P0493C11" /codon_start=1 /note="hypothetical protein" /protein_id="PRA84786_1" /db_xref="GI:606356" /translation="MWISSAVSAVAPIAGIWHYHLDASQCPNPKMIAPAFLVLRPWPHMAAFHTYKPLIUSLTVQGYSTQGLSLFDGSGRNGVORIASVODALMBRMDVACGCHFLPLGRHBSAAPTSLGSSCOPKPCNRYOFSSUPRLRANSNANGLDTISMFLARKRRENEQEGSSNVNPWMLQIDHNGSSNLISPEjoin(7961, 8199, 8666, 8937, 8962, 9033, 9134, 9205, 9487, 9558, 9770, 9841, 9937, 9962, 1010, 10098, 1016, 10169, 10254, 10322, 10440, 10511, 10637, 10708, 10792, 10863, 10948, 11019, 11102, 11173, 11262, 11333, 11448, 11519, 11611, 11682, 11795, 11866, 11963, 12034, 12124, 12195, 12272, 12353, 12398, 12515, 12601, 12732, 12838, 13176, 13259, 13329, 13761, 14114)
COMMENT	join(40, .126, 585, .819, 1979, .2001, 2924, .2946, 3836, .4073)
FEATURES	Location/Qualifiers
SOURCE	1. .143113 /organism="Oryza sativa (japonica cultivar-group)" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="P0493C11" /codon_start=1 /note="hypothetical protein" /protein_id="PRA84786_1" /db_xref="GI:606356" /translation="MWISSAVSAVAPIAGIWHYHLDASQCPNPKMIAPAFLVLRPWPHMAAFHTYKPLIUSLTVQGYSTQGLSLFDGSGRNGVORIASVODALMBRMDVACGCHFLPLGRHBSAAPTSLGSSCOPKPCNRYOFSSUPRLRANSNANGLDTISMFLARKRRENEQEGSSNVNPWMLQIDHNGSSNLISPEjoin(7961, 8199, 8666, 8937, 8962, 9033, 9134, 9205, 9487, 9558, 9770, 9841, 9937, 9962, 1010, 10098, 1016, 10169, 10254, 10322, 10440, 10511, 10637, 10708, 10792, 10863, 10948, 11019, 11102, 11173, 11262, 11333, 11448, 11519, 11611, 11682, 11795, 11866, 11963, 12034, 12124, 12195, 12272, 12353, 12398, 12515, 12601, 12732, 12838, 13176, 13259, 13329, 13761, 14114)
REFERENCE	1. (bases 1 to 1089) Subramanian, K., Abbo, S. and Deng, P.P. Isolation of two differentially expressed wheat ACC synthase cDNAs and the characterization of one of their genes with root-predominant expression
AUTHORS	Subramanian, K.
TITLE	Plant Mol. Biol. 31 (5), 1009-1020 (1996)
JOURNAL	Plant Mol. Biol. 31 (5), 1009-1020 (1996)
MEDLINE	97000913
PUBMED	8843943
REFERENCE	2. (bases 1 to 1089) Subramanian, K.
AUTHORS	Subramanian, K.
TITLE	Direct Submission
JOURNAL	Submitted (11-SEP-1995) Kuppuswamy Subramanian, USDA-ARS, Beltsville Agricultural Research Center, Plant Molecular Biology Laboratory, Beltsville, MD 20705, USA
FEATURES	Location/Qualifiers
SOURCE	1. .1089 /organism="Triticum aestivum" /clone="PwAS-1" /db_xref="taxon:4565" /EC_number="4.4.1.14" /note="ACC synthase" /codon_start=1 /product="1-aminocyclopropane-1-carboxylate synthase" /protein_id="PAB1418_1" /db_xref="GI:1173638" /translation="MGLABNHLSDLVREMMERHAGPANTPAGDEERDTLSGLATYQPGDITAKMAGFMRMORIMHSVSEPSOMWITSGATPAMEILSSCADPNAFLYPSPIYFGWDRDKWRTGELIPCRSTDNFNISITALEIYQAKKRGVRYVGVLISNPSPMTGSEPVPKDPLDUDLFRATVKNHLSIDSEFAGSDFGSEEFVSAEVNLEDFDRRHYIYGLSKDLSLAGFVYIISNEEAAKARFESVSTSTQRLVAVMLSDQKTSNLYKVNRLRKAAYNLYDQKVGICBCKFSSGGFYCWADMFSKIRSYSEKGERTLDRILKEAKNTVPESSCHIEPGW"
BASE COUNT	274 a 248 c 303 g 264 t
ORIGIN	
Query Match	36.3%; Score 146.8; DB 8; Length 1089;
Best Local Similarity	64.8%; Pred. No. 1e-35;
Matches	249; Conservative 0; Mismatches 132; Indels 3; Gaps 2;
QY	8 CGGGGTTAGGATGGGGTATCCTACTCCPACACAGAGACGTCGCTACTCCAAA 67
Db	707 CAGGGTTGAGTCAGTCAGGATCATGATTCGTTAAAGAACGATTGAGGCC 766
QY	68 AGTTGACGAGATTTCATCCATTGCTGCTCCGAGCAGCGCTTGCTGCTATGCTC 127
Db	767 AGATGCCAGATTCTCATCGTGACGCCAGGCCAGGCCCTTGTGCAAGCTT 826
QY	128 CGGACAGCGCGTTCAAAAGTCATCAGGTTAACAGAGCGAACTCAAGAATGT 187
Db	827 CGGACCCAGAAGTTTATTCGAAATTACCTGAGAGAGGGCTGGCAAGGCT 885
QY	188 ACGCGCATCGTGGCGGGGTTGAGAAACTCGCATCGATCGCAAGGAGCGGA 247
Db	887 ACAATCTGCTGCTGAT-ATGCTTGTGAGCAGGTGCGATCGTCTCAAGAGCGGA 945
QY	248 GGCTCTCATTTGTTGGCGGACATGAGCGATGATTCGATCCAGGAAAGGG 307
Db	946 GGTT--TCTACTCGTGGCGAGACAGCAGTCATCCGGTCTTACAGCGAGAAAGGAG 1003
QY	308 AGCTGAGCTATGGCAAGTGTAAACATGCTAAGGTAACAGCTACTCCGGTCTT 367
Db	1004 AGCGGAGGCTTGGCACAGGTGTTGGAGGGCGAGGCTAACGTCACCCAGSTCAT 1063
QY	368 GTTGTGTCATTGTTGAAACCCGGCT 391
FEATURES	Location/Qualifiers
SOURCE	1. .143113 /organism="Oryza sativa (japonica cultivar-group)" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="P0493C11" /codon_start=1 /note="hypothetical protein" /protein_id="PRA84786_1" /db_xref="GI:606356" /translation="MWISSAVSAVAPIAGIWHYHLDASQCPNPKMIAPAFLVLRPWPHMAAFHTYKPLIUSLTVQGYSTQGLSLFDGSGRNGVORIASVODALMBRMDVACGCHFLPLGRHBSAAPTSLGSSCOPKPCNRYOFSSUPRLRANSNANGLDTISMFLARKRRENEQEGSSNVNPWMLQIDHNGSSNLISPEjoin(7961, 8199, 8666, 8937, 8962, 9033, 9134, 9205, 9487, 9558, 9770, 9841, 9937, 9962, 1010, 10098, 1016, 10169, 10254, 10322, 10440, 10511, 10637, 10708, 10792, 10863, 10948, 11019, 11102, 11173, 11262, 11333, 11448, 11519, 11611, 11682, 11795, 11866, 11963, 12034, 12124, 12195, 12272, 12353, 12398, 12515, 12601, 12732, 12838, 13176, 13259, 13329, 13761, 14114)
COMMENT	join(40, .126, 585, .819, 1979, .2001, 2924, .2946, 3836, .4073)
FEATURES	Location/Qualifiers
SOURCE	1. .143113 /organism="Oryza sativa (japonica cultivar-group)" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="P0493C11" /codon_start=1 /note="hypothetical protein" /protein_id="PRA84786_1" /db_xref="GI:606356" /translation="MWISSAVSAVAPIAGIWHYHLDASQCPNPKMIAPAFLVLRPWPHMAAFHTYKPLIUSLTVQGYSTQGLSLFDGSGRNGVORIASVODALMBRMDVACGCHFLPLGRHBSAAPTSLGSSCOPKPCNRYOFSSUPRLRANSNANGLDTISMFLARKRRENEQEGSSNVNPWMLQIDHNGSSNLISPEjoin(7961, 8199, 8666, 8937, 8962, 9033, 9134, 9205, 9487, 9558, 9770, 9841, 9937, 9962, 1010, 10098, 1016, 10169, 10254, 10322, 10440, 10511, 10637, 10708, 10792, 10863, 10948, 11019, 11102, 11173, 11262, 11333, 11448, 11519, 11611, 11682, 11795, 11866, 11963, 12034, 12124, 12195, 12272, 12353, 12398, 12515, 12601, 12732, 12838, 13176, 13259, 13329, 13761, 14114)
REFERENCE	1. (bases 1 to 1089) Subramanian, K., Abbo, S. and Deng, P.P. Isolation of two differentially expressed wheat ACC synthase cDNAs and the characterization of one of their genes with root-predominant expression
AUTHORS	Subramanian, K.
TITLE	Plant Mol. Biol. 31 (5), 1009-1020 (1996)
JOURNAL	Plant Mol. Biol. 31 (5), 1009-1020 (1996)
MEDLINE	97000913
PUBMED	8843943
REFERENCE	2. (bases 1 to 1089) Subramanian, K.
AUTHORS	Subramanian, K.
TITLE	Direct Submission
JOURNAL	Submitted (11-SEP-1995) Kuppuswamy Subramanian, USDA-ARS, Beltsville Agricultural Research Center, Plant Molecular Biology Laboratory, Beltsville, MD 20705, USA
FEATURES	Location/Qualifiers
SOURCE	1. .1089 /organism="Triticum aestivum" /clone="PwAS-1" /db_xref="taxon:4565" /EC_number="4.4.1.14" /note="ACC synthase" /codon_start=1 /product="1-aminocyclopropane-1-carboxylate synthase" /protein_id="PAB1418_1" /db_xref="GI:1173638" /translation="MGLABNHLSDLVREMMERHAGPANTPAGDEERDTLSGLATYQPGDITAKMAGFMRMORIMHSVSEPSOMWITSGATPAMEILSSCADPNAFLYPSPIYFGWDRDKWRTGELIPCRSTDNFNISITALEIYQAKKRGVRYVGVLISNPSPMTGSEPVPKDPLDUDLFRATVKNHLSIDSEFAGSDFGSEEFVSAEVNLEDFDRRHYIYGLSKDLSLAGFVYIISNEEAAKARFESVSTSTQRLVAVMLSDQKTSNLYKVNRLRKAAYNLYDQKVGICBCKFSSGGFYCWADMFSKIRSYSEKGERTLDRILKEAKNTVPESSCHIEPGW"
BASE COUNT	274 a 248 c 303 g 264 t
ORIGIN	
Query Match	36.3%; Score 146.8; DB 8; Length 1089;
Best Local Similarity	64.8%; Pred. No. 1e-35;
Matches	249; Conservative 0; Mismatches 132; Indels 3; Gaps 2;
QY	8 CGGGGTTAGGATGGGGTATCCTACTCCPACACAGAGACGTCGCTACTCCAAA 67
Db	707 CAGGGTTGAGTCAGTCAGGATCATGATTCGTTAAAGAACGATTGAGGCC 766
QY	68 AGTTGACGAGATTTCATCCATTGCTGCTCCGAGCAGCGCTTGCTGCTATGCTC 127
Db	767 AGATGCCAGATTCTCATCGTGACGCCAGGCCAGGCCCTTGTGCAAGCTT 826
QY	128 CGGACAGCGCGTTCAAAAGTCATCAGGTTAACAGAGCGAACTCAAGAATGT 187
Db	827 CGGACCCAGAAGTTTATTCGAAATTACCTGAGAGAGGGCTGGCAAGGCT 885
QY	188 ACGCGCATCGTGGCGGGGTTGAGAAACTCGCATCGATCGCAAGGAGCGGA 247
Db	887 ACAATCTGCTGCTGAT-ATGCTTGTGAGCAGGTGCGATCGTCTCAAGAGCGGA 945
QY	248 GGCTCTCATTTGTTGGCGGACATGAGCGATGATTCGATCCAGGAAAGGG 307
Db	946 GGTT--TCTACTCGTGGCGAGACAGCAGTCATCCGGTCTTACAGCGAGAAAGGAG 1003
QY	308 AGCTGAGCTATGGCAAGTGTAAACATGCTAAGGTAACAGCTACTCCGGTCTT 367
Db	1004 AGCGGAGGCTTGGCACAGGTGTTGGAGGGCGAGGCTAACGTCACCCAGSTCAT 1063
QY	368 GTTGTGTCATTGTTGAAACCCGGCT 391
FEATURES	Location/Qualifiers
SOURCE	1. .143113 /organism="Oryza sativa (japonica cultivar-group)" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="P0493C11" /codon_start=1 /note="hypothetical protein" /protein_id="PRA84786_1" /db_xref="GI:606356" /translation="MWISSAVSAVAPIAGIWHYHLDASQCPNPKMIAPAFLVLRPWPHMAAFHTYKPLIUSLTVQGYSTQGLSLFDGSGRNGVORIASVODALMBRMDVACGCHFLPLGRHBSAAPTSLGSSCOPKPCNRYOFSSUPRLRANSNANGLDTISMFLARKRRENEQEGSSNVNPWMLQIDHNGSSNLISPEjoin(7961, 8199, 8666, 8937, 8962, 9033, 9134, 9205, 9487, 9558, 9770, 9841, 9937, 9962, 1010, 10098, 1016, 10169, 10254, 10322, 10440, 10511, 10637, 10708, 10792, 10863, 10948, 11019, 11102, 11173, 11262, 11333, 11448, 11519, 11611, 11682, 11795, 11866, 11963, 12034, 12124, 12195, 12272, 12353, 12398, 12515, 12601, 12732, 12838, 13176, 13259, 13329, 13761, 14114)
COMMENT	join(40, .126, 585, .819, 1979, .2001, 2924, .2946, 3836, .4073)
FEATURES	Location/Qualifiers
SOURCE	1. .143113 /organism="Oryza sativa (japonica cultivar-group)" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="P0493C11" /codon_start=1 /note="hypothetical protein" /protein_id="PRA84786_1" /db_xref="GI:606356" /translation="MWISSAVSAVAPIAGIWHYHLDASQCPNPKMIAPAFLVLRPWPHMAAFHTYKPLIUSLTVQGYSTQGLSLFDGSGRNGVORIASVODALMBRMDVACGCHFLPLGRHBSAAPTSLGSSCOPKPCNRYOFSSUPRLRANSNANGLDTISMFLARKRRENEQEGSSNVNPWMLQIDHNGSSNLISPEjoin(7961, 8199, 8666, 8937, 8962, 9033, 9134, 9205, 9487, 9558, 9770, 9841, 9937, 9962, 1010, 10098, 1016, 10169, 10254, 10322, 10440, 10511, 10637, 10708, 10792, 10863, 10948, 11019, 11102, 11173, 11262, 11333, 11448, 11519, 11611, 11682, 11795, 11866, 11963, 12034, 12124, 12195, 12272, 12353, 12398, 12515, 12601, 12732, 12838, 13176, 13259, 13329, 13761, 14114)
REFERENCE	1. (bases 1 to 1089) Subramanian, K., Abbo, S. and Deng, P.P. Isolation of two differentially expressed wheat ACC synthase cDNAs and the characterization of one of their genes with root-predominant expression
AUTHORS	Subramanian, K.
TITLE	Plant Mol. Biol. 31 (5), 1009-1020 (1996)
JOURNAL	Plant Mol. Biol. 31 (5), 1009-1020 (1996)
MEDLINE	97000913
PUBMED	8843943
REFERENCE	2. (bases 1 to 1089) Subramanian, K.
AUTHORS	Subramanian, K.
TITLE	Direct Submission
JOURNAL	Submitted (11-SEP-1995) Kuppuswamy Subramanian, USDA-ARS, Beltsville Agricultural Research Center, Plant Molecular Biology Laboratory, Beltsville, MD 20705, USA
FEATURES	Location/Qualifiers
SOURCE	1. .1089 /organism="Triticum aestivum" /clone="PwAS-1" /db_xref="taxon:4565" /EC_number="4.4.1.14" /note="ACC synthase" /codon_start=1 /product="1-aminocyclopropane-1-carboxylate synthase" /protein_id="PAB1418_1" /db_xref="GI:1173638" /translation="MGLABNHLSDLVREMMERHAGPANTPAGDEERDTLSGLATYQPGDITAKMAGFMRMORIMHSVSEPSOMWITSGATPAMEILSSCADPNAFLYPSPIYFGWDRDKWRTGELIPCRSTDNFNISITALEIYQAKKRGVRYVGVLISNPSPMTGSEPVPKDPLDUDLFRATVKNHLSIDSEFAGSDFGSEEFVSAEVNLEDFDRRHYIYGLSKDLSLAGFVYIISNEEAAKARFESVSTSTQRLVAVMLSDQKTSNLYKVNRLRKAAYNLYDQKVGICBCKFSSGGFYCWADMFSKIRSYSEKGERTLDRILKEAKNTVPESSCHIEPGW"
BASE COUNT	274 a 248 c 303 g 264 t
ORIGIN	
Query Match	36.3%; Score 146.8; DB 8; Length 1089;
Best Local Similarity	64.8%; Pred. No. 1e-35;
Matches	249; Conservative 0; Mismatches 132; Indels 3; Gaps 2;
QY	8 CGGGGTTAGGATGGGGTATCCTACTCCPACACAGAGACGTCGCTACTCCAAA 67
Db	707 CAGGGTTGAGTCAGTCAGGATCATGATTCGTTAAAGAACGATTGAGGCC 766
QY	68 AGTTGACGAGATTTCATCCATTGCTGCTCCGAGCAGCGCTTGCTGCTATGCTC 127
Db	767 AGATGCCAGATTCTCATCGTGACGCCAGGCCAGGCCCTTGTGCAAGCTT 826
QY	128 CGGACAGCGCGTTCAAAAGTCATCAGGTTAACAGAGCGAACTCAAGAATGT 187
Db	827 CGGACCCAGAAGTTTATTCGAAATTACCTGAGAGAGGGCTGGCAAGGCT 885
QY	188 ACGCGCATCGTGGCGGGGTTGAGAAACTCGCATCGATCGCAAGGAGCGGA 247
Db	887 ACAATCTGCTGCTGAT-ATGCTTGTGAGCAGGTGCGATCGTCTCAAGAGCGGA 945
QY	248 GGCTCTCATTTGTTGGCGGACATGAGCGATGATTCGATCCAGGAAAGGG 307
Db	946 GGTT--TCTACTCGTGGCGAGACAGCAGTCATCCGGTCTTACAGCGAGAAAGGAG 1003
QY	308 AGCTGAGCTATGGCAAGTGTAAACATGCTAAGGTAACAGCTACTCCGGTCTT 367
Db	1004 AGCGGAGGCTTGGCACAGGTGTTGGAGGGCGAGGCTAACGTCACCCAGSTCAT 1063
QY	368 GTTGTGTCATTGTTGAAACCCGGCT 391
FEATURES	Location/Qualifiers
SOURCE	1. .143113 /organism="Oryza sativa (japonica cultivar-group)" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="P0493C11" /codon_start=1 /note="hypothetical protein" /protein_id="PRA84786_1" /db_xref="GI:606356" /translation="MWISSAVSAVAPIAGIWHYHLDASQCPNPKMIAPAFLVLRPWPHMAAFHTYKPLIUSLTVQGYSTQGLSLFDGSGRNGVORIASVODALMBRMDVACGCHFLPLGRHBSAAPTSLGSSCOPKPCNRYOFSSUPRLRANSNANGLDTISMFLARKRRENEQEGSSNVNPWMLQIDHNGSSNLISPEjoin(7961, 8199, 8666, 8937, 8962, 9033, 9134, 9205, 9487, 9558, 9770, 9841, 9937, 9962, 1010, 10098, 1016, 10169, 10254, 10322, 10440, 10511, 10637, 10708, 10792, 10863, 10948, 11019, 11102, 11173, 11262, 11333, 11448, 11519, 11611, 11682, 11795, 11866, 11963, 12034, 12124, 12195, 12272, 12353, 12398, 12515, 12601, 12732, 12838, 13176, 13259, 13329, 13761, 14114)
COMMENT	join(40, .126, 585, .819, 1979, .2001, 2924, .2946, 3836, .4073)
FEATURES	Location/Qualifiers
SOURCE	1. .143113 /organism="Oryza sativa (japonica cultivar-group)" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="P0493C11" /codon_start=1 /note="hypothetical protein"<

QY	128	CGGACACGGGGTCACTCAAAAGTCATCGGAGTAACAGACGGAACTCAGAAGATG	187
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QY	188	ACGCTCATGTTGGGGGCTTGAAGAACCTCGGATCCATGGACGGAAAGCAGCGGA	247
Db	34909	ACCATTTGTTGTTGATGCTTGGATCACTGGGATTAGTCAGACAGAGCAGTGA	34967
QY	248	GGCTCTCTATGTTGGCGACATGAGCGATGTTGATTCAGCAGAAAGAG	307
Db	34958	GGGT--TCTACTGCTGGCACAGCATGAGCAAGTTCATCAGGCTTACAGCGAAGAGGG	35025
QY	308	ACCTGAGCTATGGGACAACTGCTAACATTGCTTAAACGTTACTCCGGTCT	367
Db	35026	AGCGCACTGTTGGAGTAGGTATTGGAGGAGCAAGGTCAATGTCACTCCAGGTCT	35085
QY	368	GTGTGATGTTGATGACCCGCTACTT	398
Db	35086	CCTGCCATTGATCGAGCTGGATGGTCAG 35116	
RESULT 8			
LOCUS	AF336920	AF336920	1488 bp mRNA linear PLN 18-APR-2002
DEFINITION	Arabidopsis thaliana 1-amino cyclopropane-1-carboxylate synthase		
ACCESSION	AF336920	(At5g1690)	mRNA, complete cds.
VERSION	AF336920.1	GI:12484204	
KEYWORDS	FLL,CDNA:Arabidopsis thaliana.		
SOURCE	Arabidopsis thaliana.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Rosidae; eurosid II; Brassicales; Brassicaceae; Arabidopsis. (bases 1 to 1488)		
AUTHORS	Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Arabidopsis open Reading Frame (ORF) Clones		
JOURNAL	unpublished		
REFERENCE	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Kallin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.		
AUTHORS	Direct Submission		
JOURNAL	Submitted (17-JAN-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA		
FEATURES	source		
REFERENCE	1. .1488		
AUTHORS	/organism="Arabidopsis thaliana"		
NOTE	/db_xref="Taxon:3702",/chromosome="5",/clone="C00056"		
NOTE	"This clone is in pUNI-T3-D/V5-His-TOPO. ecotype: Columbia"		
gene	1. .1488		
NOTE	/evidence=experimental		
CDS	1. .1488		
NOTE	/gene="At5g1690"		
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NOTE	/codon_start=1		
NOTE	/product="1-amino cyclopropane-1-carboxylate synthase		
NOTE	/product_id="AAG54001.1"		
NOTE	/db_xref="GI:12484205"		
NOTE	/translation="MRLIVPLPGVIGRGLFVGSILPCCFLYFLQYKRRRPPSD		
NOTE	PTDLPFRSRINIFSRGNSIGRVSSEAVPKPSDPSVYIGLERKTDPRDINT		
NOTE	DTQIQLAEESTCFLDQWNLINMMSMDDGDRDISSIMAMYVPEFGLELR		
RESULT 9			
LOCUS	AB010074	AB010074	86212 bp DNA linear PLN 27-DEC-2000
DEFINITION	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: M1024.		
ACCESSION	AB010074	BA00015	
VERSION	AB010074.2	GI:10177866	
KEYWORDS			
SOURCE	Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1 clone:M1024.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 (sites)		
AUTHORS	Sato, T., Kaneko, T., Kotani, H., Nakamura, Y., Asamizu, E., Miyajima, N. and Tabata, S.		
TITLE	Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456-315 bp covered by nineteen physically assigned P1 and TAC clones		
JOURNAL	DNA Res. 5 (1), 41-54 (1998)		
MEDLINE	98295056		
REFERENCE	2 (bases 1 to 86212)		
AUTHORS	Nakamura, Y.		
JOURNAL	Submitted (07-JAN-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel:81-438-52-3955, Fax:81-438-52-3934)		
COMMENT	On Sep 15, 2000 this sequence version replaced gi:2760170.		
NOTE	Address for correspondence: ynakamu@kazusa.or.jp		
NOTE	For the latest information on annotation of this clone, please see		
BASE COUNT			
ORIGIN	386 a	289 c	359 g
ORIGIN	454 t		
Query Match			
Best Local Similarity	60.8%	Score 127.6;	DB 8;
Matches	243;	Pred. No. 1	6e-29;
Conservative	0;	Mismatches	154;
		Indels	3;
		Gaps	2;
QY	5	TCCCGGGTTAGGATGGCGTTATCTACTCTTACACGAGCTCTACTCCCA	64
Db	1013	TTCCTGGTTAGAGCTCATCTACTCCCTCATGAAGCTAGTGTAGTAATGCGAA	1072
QY	65	AAAGTTCAGGAGATTCATCATTCTAGCCGTCGAGGAGCAGCAGAACTCAARAGAA	184
Db	1073	AGAACGTCATGAGATTCATCAGTCGCGACTCTAGTCAGTCAAAAGGATA	1132
QY	125	TCTCGACACGGGTTACTCAARAGTCATCGGAGTACATGCGACAGCAGAAAGGATCCGGGATA	1192
Db	1133	TATCTGATGTAAGATCATCTGGGGATACATGCGACAGCAGAAAGGATCCGGGATA	1192
QY	185	TGTCAGCTGCAATTCGTCGGGGGTGAGAAACTCGCATCCGATGCGACGGAAAGGAGC	244
Db	1193	AGCATATTGGTTGGG-AAGTTGAAACATTAGGATACCATGTCGAGAGGAGGT	1251
QY	245	GGGGCTCTCTCATTTGTTGGGGCACTAGTGTAGGATGATGATGATCTTACAGTCCTACASCGGAAAG	304
Db	1252	GGTGGGTT-TGTATTGTTGGTGTAGCATGAGCTTACTGACATCTACAGTGTAGAAG	1309
QY	305	GAGGCTCGAGCTATGGGACAGTTGCTAACATTGCTTAAGGAAAGCTTACCTCCGTT	364
Db	1310	GAGAACCTGGATTATGAGAAGCTATGACTGTGTGCTAAGATTAATGCCACTCCGAA	1369
QY	365	CTGTGTCATGTTAGAACCCGGCACTTGTACCTCTG 404	
Db	1370	CAGCTGTATGTTAGAACCCAGGTGGTCAGGTCTG 1409	

FEATURES	Source	Location/Qualifiers
ORIGIN		/codon_start=3 /product="ACC synthase" /protein_id="AA28795.1"
BASE COUNT	379 a 365 c 310 g 346 t	Query Match 27.4%; score 110.8; DB 8; Length 1400; Best Local Similarity 57.9%; Pred. No. 3.9e-24; Matches 234; Conservative 0; Mismatches 167; Indels 3; Gaps 2;
old_sequence		QY 1 GGGTGGCCGGGGTCAGGATGGGGTATATCTACTCTACAGAGACGGCTCACT 60 Db 789 GGCCCTCCGGTTTCGAGTGGCCCATCTTCAACGACAGTGGTGGCCGC 848 QY 61 GCCAAAAGGTGACCATTTTCATCCATTCAGCTCGAGGACGGCTTGCTCGRGT 120 Db 849 GCTACAAAGATGTCAGCTTGGCTCTCCAACTCGACCTCTCCGCC 908 QY 121 ATGCTCTGGACACGGGTTACTCAAGAATCATCGAGGAAACAGGAACTCAA 180 Db 909 ATGCTATCCAAACAAACTACTAACATAGCCGAAACAAAGACTCAA 968 QY 181 AGATGTACGCTGCATTCGGGGGGTGAAGAAACTCGGATCCGAGCAGGAAG 240 Db 969 CAACGTCAGAAAAGCTCGTCGCCCTT-CGAAATCTGGCATTAAGCTCACGG 1027 QY 241 CAGCGGAGGCTCTCTATTGGCCGACATGAGGGATGATGATGATCCTACAGGAA 300 Db 1028 CAATGCTGGCT-TGTCCTGGGATGAGGCACTTGCTTAGGTCACRCTT 1085 QY 301 AAAGGAGAGCTGGAGTATGGACAAGTTCTAAACATTGCTAAAGTAAAGCTTACGCC 360 Db 1086 GAAGCCGAAATGAGCTCTGGAAAGATGATGATGAGGATTCACCTCATATACTCCT 1145 QY 361 GCTTCCTGTGTCATGTATGAAACCCGCTACTTTAGCCTCTG 404 Db 1146 GGATCGHCTGTCATWGACCGAACCTGGTGGTCCGGTCTG 1189
BASE COUNT	437 a 398 c 351 g 432 t	Query Match 27.4%; score 110.8; DB 8; Length 1618; Best Local Similarity 57.9%; Pred. No. 4e-24; Matches 234; Conservative 0; Mismatches 167; Indels 3; Gaps 2;
CDS		QY 1 GGGTGGCCGGGGTCAGGATGGGGTATATCTACTCTACAGAGACGGCTCACT 60 Db 799 GGCCCTCCGGTTTCGAGTGGCTCTCTCAACTCAGCACCTCTCCGCC 918 QY 121 ATGCTCTGGACACGGGTTACTCAAGAATCATCGAGGAAACAGGAACTCAA 180 Db 919 ATGCTATCCGACAAACTACTAACATAGCCGAGACACAAAGACTCAA 978 QY 181 AGATGTACGCTGCATTCGGGGGGTGAAGAAACTCGGATCCGATGACGGAAAG 240 Db 979 CAACGTCAGAAAAGCTCTCGGCCCT-CGAAATCTGGCATAGCTGCTCACGG 1037 QY 241 CAGCGGAGGCTCTCTATTGGCCGACATGAGGGATGATGATGATCCTACAGGAA 300 Db 1038 CAATGCTGGCT-TGTCCTGGTGGGATATGAGGCACTTGCTTAGGTCACRCTT 1095 QY 301 AAAGGAGAGCTGGAGTATGGACAAGTTCTAAACATTGCTAAAGTAAAGCTTACGCC 360 Db 1096 GAAGCGAAATGAGCTCTGGAAAGATGATGAGGATTCACCTCATATCCT 1155 QY 361 GGTTCCTGTGTCATGTATGACCCGGCTACTTACGCC 404 Db 1156 GGATCGHCTGTCATWGACCGAACCTGGTGGTCCGGTCTG 1199
RESULT 13		
LOCUS	MSU03294	1618 bp mRNA linear PLN 18-NOV-1993
DEFINITION	Malus sylvestris 1-aminocyclopropane-1-carboxylate synthase mRNA.	
ACCESSTION	U03294	Partial cds.
VERSTON	003294.1	GI:417971
KEYWORD		
SOURCE		
ORGANISM	Malus sylvestris.	
REFERENCE		Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
AUTHORS	Dong, J.G., Kim, W.T., Yip, W.K., Thompson, G.A., Li, L., Bennett, A.B.	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Malus sylvestris.
JOURNAL	Plantae 185, 38-45 (1991)	
REFERENCE	Dong, J.G.	Cloning of a cDNA encoding 1-aminocyclopropane-1-carboxylate synthase and expression of its mRNA in ripening apple fruit
AUTHORS	2 (bases 1 to 1618)	
TITLE		
JOURNAL	Submitted (9-Nov-1993) Jian G. Dong, 'Vegetable crops', University of California at Davis, Mann Lab, Davis, CA 95616-8631, USA	
REFERENCE	Dong, J.G.	
AUTHORS		
TITLE		
JOURNAL		
RESULT 14		
LOCUS	MD0011518	1633 bp DNA linear PLN 23-OCT-1998
DEFINITION	Malus domestica acc synthase gene, exons 1-4, partial.	
ACCESSTION	AJ011518	
VERSION	AJ011518.1	1-aminocyclopropane-1-carboxylic synthase; acc synthase gene.
KEYWORDS		
SOURCE		
ORGANISM	Malus x domestica.	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

ORIGIN

Query Match Similarity 27.4%; Score 110.8; DB 8; Length 1778;
 Best Local Similarity 57.9%; Pred. No. 4e-24; Mismatches 0; Matches 234; Conservative 234; Indels 3; Gaps 2;

QY 1 GGCTTGCAGGGTTCTAGATGGGTTATCTACTCTTACACAGGAGACGTCTCACTACT 60
 Db 912 GGCCTTCGGGTTTCGGGTTGGCCATTACTCCACAGGAGACAGGTTGGCCGCC 971

QY 61 GCGAAAAAGTTGAGGATTTCATCCATTGAGCTCCGACCGAGCCTGGTGTGGT 120
 Db 972 GCTACAAAATGTCACGTTGGTCTGTTCTCAAACUTGACACTCTCCGCC 1031

QY 121 ATGCTTCCTGGACAGCGCGTTCACTCAAAGTTCATCGAGGTAACAGAGCGAACAGCAA 180
 Db 1032 ATGCTTATCGACAGAAACTCACTAAGACTACAGTACAGTAGCCGAGAACACAAAGCICAA 1091

QY 181 AGANTGAGCCTCATTGGGGGGTGAAGAACTCGGCATCGCGATGACGGAAAG 240
 Db 1092 CAACGTCAGAAAATCTCGTCCTCGGCCCT-CAGAAAGCTGGCATTAAGCTGCTCAAATGG 1150

QY 241 CAGGGGAGGCTCTCATATGTTGGCCACATGAGCGGATGATCGATCCPACAGCGA 300
 Db 1151 CAACTGCTGCT- TGTTCCTGTTGGTGGATATGGGACTTGCTTAGTCACACCTTT 1208

QY 301 AAAGGAGAGCTCGAGCTATGGGACAAAGTGTCAAACATTTGTAACGTTAACGTTACTCC 360
 Db 1209 GAAAGCCGAAATGGAGCTCTGGAAAAGATTGATACGGAGTCACCTCAATTCCTCT 1268

QY 361 GGTTCTGTTGTCATTTGTTGACCCGCTACTTTAGCTCTCTG 404
 Db 1269 GGATCTGCTCTGTCAGGACCTGTTGGTCCGTCTG 1312

Search completed: March 11, 2003, 01:20:16
 Job time : 1686 secs

Run on:	March 11, 2003, 00:41:37 ; Search time 1211 Seconds (without alignments) 5402.953 Million cell updates/sec
Perfect score:	US-09-975-842-1
Sequence:	1 gggttgcgggggttcaggat.....ccggctacttttagcctctg 404
Scoring table:	IDENTITY-NUC Gapop 10.0 , Gapext 1.0
Searched:	16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters:	32308132
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	EST:*
	1: em_estba:*
	2: em_estbhum:*
	3: em_estin:*
	4: em_estinu:*
	5: em_estrov:*
	6: em_esttp1:*
	7: em_estro:*
	8: em_htc:*
	9: gb_est1:*
	10: gb_est2:*
	11: gb_htc:*
	12: gb_est3:*
	13: gb_est4:*
	14: gb_est5:*
	15: em_estfun:*
	16: em_estom:*
	17: gb_gss:*
	18: em_gss_hum:*
	19: em_gss_inv:*
	20: em_gss_pln:*
	21: em_gss_vrt:*
	22: em_gss_fun:*
	23: em_gss_main:*
	24: em_gss_mus:*
	25: em_gss_other:*
	26: em_gss_pro:*
	27: em_gss_rnd:*
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Result No.	Query Match length DB ID
	Description
	SUMMARIES
REFERENCE	RESULT 1
LOCUS	BM437295
DEFINITION	VWA017C10 54085 An expressed sequence tag database for abiotic stressed leaves of <i>Vitis vinifera</i> var. Chardonnay <i>Vitis vinifera</i> CDNA clone VWA017C10 5, mRNA sequence.
ACCESSION	BM437295
VERSION	BM437295.1
KEYWORDS	EST
SOURCE	<i>Vitis vinifera</i> .
ORGANISM	Bukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; <i>Vitis</i>
COMMENT	1 (bases 1 to 664) Cramer, G.R. and Cushman, J.C.
JOURNAL	Unpublished (2002)
AUTHORS	Department of Biochemistry University of Nevada Reno, NV 89557-0014, USA
TITLE	An expressed sequence tag database for abiotic stressed leaves of <i>Vitis vinifera</i> var. Chardonnay
FORWARD:	T3 20mer
BACKWARD:	T7 21mer

FEATURES	source	BASE COUNT	195	a	119	c	152	g	197	t	1	others	ORIGIN
Query Match													
Best Local Similarity	48.2%	Score	194.8	DB	13	Length	664						
Matches	285	Pred.	No. 2e-55	Indels	112	Gaps	3						
QY	5	TGCCGGGGTCAAGATGGCGTATCACTCTACACGAGACGCTACTACGCCA	64	Db	36	TTCCAGTTAACGGGGTATATATCGTCTATGAAATGTTCTGCTGCTGCTA	95						
QY	65	AAAAGTGTGAGGATTTCTCCATTCAGCTGCCAGCGAGGCTTCTCGTGTATGC	124	Db	96	AGAACTCTCAAGTTCTCCATTCAGCTGCCAACCCAGTGTGTTCTCCATGC	155						
QY	125	TCTCGGACACCGGGTCACTTAAAGTCACTGAGGAACAGAGCCAACTCAAGAA	184	Db	156	TTCAGATATAGATTATACAAAGTCTATCAGACCAACAGAGAGCTCAAGAA	215						
QY	185	TGTACGTCGATCGGGGGTGAAGAACACTCGCATCGATGCCAACGAGC	244	Db	216	TGTATACTAAATCGTGC-AGGTGAAACATATTAGATTAGTGTAGTCATGCGAGC	274						
QY	245	GGAGGCTTCTCTAATGTTGGCGACATGGGGATGATGATCCTACAGGAAAG	304	Db	275	GGGGCTT-TCTACTGTGTTGGTACATGGGGATTAACTCGCTCTACATGAGAAG	332						
QY	305	GAGAGCTCGAGSTGGAGCAAGTGTCTAACATTGTAGGAAAGCTACGCCGT	364	Db	333	GGAGCTCGAGCTGAGTGGACAAATGTGAATATGAGATAATGTAATCCAGGT	392						
QY	365	CTGTCTCATGATGAGAACCGGCTACTTGTAGCCCTG	404	Db	393	CTCTGTGACTGTATGAGACCGGATGTTCCGCTGTTG	432						
RESULT	2												
LOCUS	BF425479												
DEFINITION	su56c02.y1 Gm-c1069 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1069-591		503	bp	mRNA	linear	EST	06-DEC-2001					
ACCESSION	GM-C1069-591												
VERSION	BF425479												
KEYWORDS	EST.												
SOURCE	soybean.												
ORGANISM	Glycine max												
REFERENCE	1 (bases 1 to 503)												
AUTHORS	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.												
COMMENT													
FEATURES	source	BASE COUNT	116	a	86	c	134	g	167	t			ORIGIN
Query Match													
Best Local Similarity	43.1%	Score	174	DB	12	Length	503						
Matches	272	Pred.	No. 2.5e-48	Indels	125	Gaps	3						
QY	5	TGCCGGGGTTCAGGTGGGGTTACCTACTCCTACAGAACGAGACCTGCTACTACGCCA	64	Db	37	TTCCGAGTTGAGGTGGGTATCTACTCTTATATGACATGTCGTCGCTGCTCTTCGA	96						
QY	65	AAAGTTGAGGAGATTCTCCATTCAGCTGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTG	124	Db	97	GCAATTGGCAAGGTTCTCCACTGTTGCCCCACCCAAAGATGTCATCTCCATGC	156						
QY	125	TCTCGACACCGGTTCACTCAAAAGTCATCGAGTAACAGAGGAACACTCAAAGAA	184	Db	157	TTTCGATACAGTAAATTGTCGCAAATTAATTGAGGTTAACAGGTGTAGGCTGGCGAAA	216						
QY	185	TGTAGCTGCTGATTCGGGGGGTGAAGAACACTCGGATCCTCGATGTCAGGAGCAGC	244	Db	217	TGTATAATACATGTTGTCGGGGCTGAGCACTGGGGATTGTGACTAGGGCACT	275						
QY	245	GGAGCTCTCATGTTGGCCACATGAGGGTTGATGTCAGTACAGCGAAAG	304	Db	276	GGTGG-TTGTGCTGGCTGCTGAGCATGAGCAGGTGTTCTACAGTGTGAAAG	333						
QY	305	GAGACTCGAGCTATGGACAGTGTCAACATGCTAGGTAAACGTTACTCCGGTT	364	Db	334	GAGACTCTGAGCTGGGGATAGATGTTGATGTTGCTAAGTCAATGTTACCCGGGT	393						
QY	365	CTTGTGTCATGTGTTGAACCTGGATGTTGCTGTTG	404	Db	394	CTTGTGTCATGTGTTGAACCTGGATGTTGCTGTTG	432						

FEATURES	Source	Location/Qualifiers	
BASE COUNT	193 a	Location/Qualifiers 1. .685	
ORIGIN	163 c	Location/Qualifiers /organism="Arabiopsis thaliana" <db_xref="taxon:3702" <clone="RAFL04-20-B08" <note="Site_1: SstI; Site_2: XbaI; subjected to cold-treated(1,2,5,10,24 hr)" /lab_host="SOLR"	
Query Match	36.6%; Score 147.8; DB 10; Length 685; Best Local Similarity 63.8%; Pred. No. 2.8e-39; Matches 256; Conservative 0; Mismatches 142; Indels 3; Gaps 2;	Query Match	36.0%; Score 147.8; DB 10; Length 685; Best Local Similarity 63.8%; Pred. No. 2.8e-39; Matches 256; Conservative 0; Mismatches 142; Indels 3; Gaps 2;
QY	4 TGGCGGGGTTGAGATGGCGTTATCCTACTCTACACAGGAGCGTCACTTGCC 63	QY	4 TGGCGGGGTTGAGATGGCGTTATCCTACTCTACACAGGAGCGTCACTTGCC 63
Db	529 TCTCGGGGCTTGTAGATCGCTGCTATCCTACTCTGCTTCACAGGAGGTGTTATCGCTTCAG 470	Db	529 TCTCGGGGCTTGTAGATCGCTGCTATCCTACTCTGCTTCACAGGAGGTGTTATCGCTTCAG 470
QY	64 AAAAGTGTGACGGATTTCATCCATTTCAGCTCCAGGAACTCAAAGA 123	QY	64 AAAAGTGTGACGGATTTCATCCATTTCAGCTCCAGGAACTCAAAGA 123
Db	469 AGAACGCTACGAGCTTCACCTGTCATCACAACCAACATTGCTGATATCCGCA 410	Db	469 AGAACGCTACGAGCTTCACCTGTCATCACAACCAACATTGCTGATATCCGCA 410
QY	124 CTCCTGGACACGGGGTTCACTCAAAGTCTACGAGGAACTCAAAGA 183	QY	124 CTCCTGGACACGGGGTTCACTCAAAGTCTACGAGGAACTCAAAGA 183
Db	409 ATCTCCAATCAAATAATGTCAGAGATTGTAAGAACACAGGAGATGAGT 350	Db	409 ATCTCCAATCAAATAATGTCAGAGATTGTAAGAACACAGGAGATGAGT 350
QY	184 ATGACCTGTCATGCGGGGTTGAGAACACTGGCATCGTGGACGGAAACAG 243	QY	184 ATGACCTGTCATGCGGGGTTGAGAACACTGGCATCGTGGACGGAAACAG 243
Db	349 ATCTACAGGAGCTCGTG-AGGGTGAAGAGTAGGGATCGAGTCACAGAGCA 291	Db	349 ATCTACAGGAGCTCGTG-AGGGTGAAGAGTAGGGATCGAGTCACAGAGCA 291
QY	244 CGAGGCTTCCTATGTTGGCCGAGATGACGGGATGATCGATCTACGGAAA 303	QY	244 CGAGGCTTCCTATGTTGGCCGAGATGACGGGATGATCGATCTACGGAAA 303
Db	290 TGGAGGT-TCTACTGTGGGTGATATCGAGGATGATTCATCTACAGGAAAA 233	Db	290 TGGAGGT-TCTACTGTGGGTGATATCGAGGATGATTCATCTACAGGAAAA 233
QY	304 GGAGAGCGCAGACATGAGCTTGCTAACATGCTTAAGTAACTGTTACTCCGGT 363	QY	304 GGAGAGCGCAGACATGAGCTTGCTAACATGCTTAAGTAACTGTTACTCCGGT 363
Db	232 GGCGAGATTGAGCTGTGAGAACAGCTGTGAACTCATGTCATAACCGAGA 173	Db	232 GGCGAGATTGAGCTGTGAGAACAGCTGTGAACTCATGTCATAACCGAGA 173
QY	364 TCTTGTCTGATGACCCGGTACTTTAGCTCTG 404	QY	364 TCTTGTCTGATGACCCGGTACTTTAGCTCTG 404
Db	172 TCTTGTCTGACTGTATGACACGAGATGGTTCGGTACTG 132	Db	172 TCTTGTCTGACTGTATGACACGAGATGGTTCGGTACTG 132
RESULT 7		RESULT 7	
LOCUS	BM93903	LOCUS	BM93903
DEFINITION	sam67f01_y1 Gm-c1069 Glycine max mRNA clone ID: Gm-c1069-448	DEFINITION	sam67f01_y1 Gm-c1069 Glycine max mRNA clone ID: Gm-c1069-448
ACCESSION	BM93903	ACCESSION	BM93903
VERSION	1	VERSION	1
KEYWORDS	EST.	KEYWORDS	EST.
SOURCE	soybean.	SOURCE	soybean.
ORGANISM	Glycine max	ORGANISM	Glycine max
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.		
REFERENCE	1 (bases 1 to 550)	REFERENCE	1 (bases 1 to 550)
AUTHORS	Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Boilla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Smaller, T., Gibbons, M., Pape, D., Harvey, N., Schlueter	AUTHORS	Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Boilla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Smaller, T., Gibbons, M., Pape, D., Harvey, N., Schlueter
BASE COUNT	169 a	BASE COUNT	169 a
ORIGIN	135 c	ORIGIN	135 c
Query Match	36.0%; Score 145.6; DB 14; Length 550; Best Local Similarity 63.4%; Pred. No. 1.5e-38; Matches 255; Conservative 0; Mismatches 144; Indels 3; Gaps 2;	Query Match	36.0%; Score 145.6; DB 14; Length 550; Best Local Similarity 63.4%; Pred. No. 1.5e-38; Matches 255; Conservative 0; Mismatches 144; Indels 3; Gaps 2;
QY	3 GTGCCGGGGTCAGATGGCGTATCTACTCTACAGAGAACGCTGCTACTAGTC 62	QY	3 GTGCCGGGGTCAGATGGCGTATCTACTCTACAGAGAACGCTGCTACTAGTC 62
Db	431 GCTGTGCTGCTTAGAGTGGGGTTAAAGTCTCATGAGAGTAGCTGTTGCTGC 372	Db	431 GCTGTGCTGCTTAGAGTGGGGTTAAAGTCTCATGAGAGTAGCTGTTGCTGC 372
QY	63 CAAAAGTGTGACAGATTTCACTTCGTCGACGGCTGCTGTTGCTGTTGCTG 122	QY	63 CAAAAGTGTGACAGATTTCACTTCGTCGACGGCTGCTGTTGCTGTTGCTG 122
Db	371 CAGAAAGTGTGAGATTTCCTCTATCCGTCGACGGCTGCTGTTGCTGTTG 312	Db	371 CAGAAAGTGTGAGATTTCCTCTATCCGTCGACGGCTGCTGTTGCTGTTG 312
QY	123 GCTGTCGACAGCGGGTTCACCTCAAATTCATCGAGGTTAACAGCCAACTCAAAG 182	QY	123 GCTGTCGACAGCGGGTTCACCTCAAATTCATCGAGGTTAACAGCCAACTCAAAG 182
Db	311 GCTTCAGATAAAGATTTCTGGAGTACTTGTGAGGATTCAGAACACGAGAAATACGCA 252	Db	311 GCTTCAGATAAAGATTTCTGGAGTACTTGTGAGGATTCAGAACACGAGAAATACGCA 252
QY	183 ATGTAAGTGTGATTCGGGGGGTTGAGAACACTCGGCATCCGGATCGGAAAGA 242	QY	183 ATGTAAGTGTGATTCGGGGGGTTGAGAACACTCGGCATCCGGATCGGAAAGA 242
Db	251 AGTCACGATGATGTTGGT-GTTGTTAAAGTAACTAGTAGAATCGTCAAGTGGCA 193	Db	251 AGTCACGATGATGTTGGT-GTTGTTAAAGTAACTAGTAGAATCGTCAAGTGGCA 193
QY	243 GCGGAGGTCTCTATGTTGGCCGACATGAGCGGTTAGTGTGCTCTACAGCGAAA 302	QY	243 GCGGAGGTCTCTATGTTGGCCGACATGAGCGGTTAGTGTGCTCTACAGCGAAA 302
Db	192 GCTGCTG--TATGTAAGTGGTGGCTGATAGTGGTTAATCTCG 135	Db	192 GCTGCTG--TATGTAAGTGGTGGCTGATAGTGGTTAATCTCG 135
QY	303 AGAGAACTCTGGAGTGGAGAAGTGTAACTAGTGTAGTAACTGTTACTCCGG 362	QY	303 AGAGAACTCTGGAGTGGAGAAGTGTAACTAGTGTAGTAACTGTTACTCCGG 362
Db	134 AGGAGAAATTGATTGATGGAGAGTTTGTGTTGCTGATAGTAACTCTCG 75	Db	134 AGGAGAAATTGATTGATGGAGAGTTTGTGTTGCTGATAGTAACTCTCG 75
QY	363 TCTTGTGTTGAGTGTGACCCGGCTACATTAGTGGCTCTG 404	QY	363 TCTTGTGTTGAGTGTGACCCGGCTACATTAGTGGCTCTG 404
Db	74 GTCAGGCTGCAATGCAAGAACAGGATGGTTAGGATG 33	Db	74 GTCAGGCTGCAATGCAAGAACAGGATGGTTAGGATG 33

RESULT 8		RESULT 9	
LOCUS	DEFINITION	LOCUS	DEFINITION
BJ447315	BJ447315 629 bp mRNA linear EST 23 MAY-2002	BJ209956	BE209956 so3b07.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1039-110' 5'
DEFINITION	vegetative stage leaves <i>Hordeum vulgare</i> subsp. <i>vulgare</i> cDNA clone	DEFINITION	1-AMINOCYCLOCOPROPANE 1-CARBOXYLATE SYNTHASE ; mRNA sequence.
ACCESSION	BJ447313	ACCESSION	BE209956.1 GI:8826235
VERSION	BJ447315.1 GI:21125948	VERSION	EST.
KEYWORD		KEYWORD	soybean.
SOURCE		ORGANISM	Fukuyuta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
ORGANISM		REFERENCE	Glycine.
REFERENCE	1 (bases 1 to 629); Sato, K., Saito, D. and Takeda, K., Barley EST sequencing project in NIG and Okayama Univ Unpublished (2001)	AUTHORS	1 (bases 1 to 410); Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steeple, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
AUTHORS		TITLE	Public Soybean EST Project
TITLE		COMMENT	Unpublished (1999) Contact: Shoemaker R/Public Soybean EST Project
JOURNAL		COMMENT	Public Soybean EST Project
JOURNAL		COMMENT	Washington University School of Medicine
COMMENT		COMMENT	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
COMMENT		COMMENT	Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
COMMENT		COMMENT	This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35001 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
COMMENT		COMMENT	Insert Length: 1204 Std Error: 0.00
COMMENT		COMMENT	High quality sequence stop: 409.
FEATURES		FEATURES	Location/Qualifiers
SOURCE		SOURCE	1. .629
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SOURCE		SOURCE	/cultivar="Akashiniriki"
FEATURES		FEATURES	/db_xref="taxon:112509"
SOURCE		FEATURES	/clone="baaki403"
FEATURES		SOURCE	/clone_lib="K. Sato unpublished cDNA library, cv. Akashiniriki vegetative stage leaves"
SOURCE		FEATURES	/tissue_type="leaves"
FEATURES		SOURCE	/dev_stage="vegetative stage"
SOURCE		FEATURES	
BASE COUNT	165 a 139 c 174 g 151 t	BASE COUNT	1. .629
ORIGIN		ORIGIN	
FEATURES		FEATURES	Best Local Similarity 63.8%; Score 143.6; DB 13; Length 629; Matches 250; Conservative 0; Mismatches 139; Indels 3; Gaps 2;
SOURCE		SOURCE	Best Local Similarity 63.5%; Score 143.6; DB 13; Length 629; Matches 250; Conservative 0; Mismatches 139; Indels 3; Gaps 2;
FEATURES		FEATURES	Best Local Similarity 63.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
SOURCE		SOURCE	Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
BASE COUNT	97 a 72 c 110 g 130 t	BASE COUNT	97 a 72 c 110 g 130 t
ORIGIN		ORIGIN	
FEATURES		FEATURES	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
SOURCE		SOURCE	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
BASE COUNT	241 -TCCTACTGGCGGGATAGACCACTTCATCGGCTTACAGCAGAAGGCC	BASE COUNT	241 -TCCTACTGGCGGGATAGACCACTTCATCGGCTTACAGCAGAAGGCC
ORIGIN		ORIGIN	
FEATURES		FEATURES	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
SOURCE		SOURCE	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
BASE COUNT	313 GACCTATGGACAGTGTCTAACATGCTAACGGTAAGGTACTCCGGTCTGTGTC	BASE COUNT	313 GACCTATGGACAGTGTCTAACATGCTAACGGTAAGGTACTCCGGTCTGTGTC
ORIGIN		ORIGIN	
FEATURES		FEATURES	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
SOURCE		SOURCE	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
BASE COUNT	300 AGCTTGGAGCGCTTGAGGAGGCCAATGTCACCCAGGTCATCTGC	BASE COUNT	300 AGCTTGGAGCGCTTGAGGAGGCCAATGTCACCCAGGTCATCTGC
ORIGIN		ORIGIN	
FEATURES		FEATURES	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
SOURCE		SOURCE	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
BASE COUNT	373 CATGGTACGGCCACTTGTAGCTCTG 404	BASE COUNT	373 CATGGTACGGCCACTTGTAGCTCTG 404
ORIGIN		ORIGIN	
FEATURES		FEATURES	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
SOURCE		SOURCE	Query Match 34.7%; Score 140; DB 10; Length 410; Best Local Similarity 68.4%; Score 140; DB 10; Length 410; Matches 223; Conservative 0; Mismatches 100; Indels 3; Gaps 2;
BASE COUNT	360 CATGGTACGGCTGGTTAGGCTG 391	BASE COUNT	360 CATGGTACGGCTGGTTAGGCTG 391

/dev_stage="4-6 week old plants"
 /lab_host="XLI-Blue MRF"
 /note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2: XbaI; cIET - inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, ETX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning." EcoRI
 BASE COUNT 135 a 68 c 126 g 154 t
 ORIGIN
 Query Match 29.2%; Score 118; DB 10; Length 483;
 Best Local Similarity 66.9%; Pred. No. 4 1e-29;
 Matches 198; Conservative 0; Mismatches 95; Indels 3; Gaps 2;
 QY 103 CAGCCTCTGGTGTGTTGTTGCTCGGACAGCGGTCACTCAAAGTTCATCCAGGTA 162
 Db 1 CAGAGCTTATAGTGTGCAATGCTTCAGATGCTGGTTCAAGATATAGAGACA 60
 QY 163 AACAGAGGAACTCAAAGATGTCAGCTCCATCGTGGCGGGTGAAGAACCTGG 222
 Db 61 AACAGAGAGATGTCGCGCAAGTGTGTTGACTTGTGGCGAGGCTAAACANT-TGG 119
 QY 223 CATCCGATGGACGGAAAGCAGCGGGCTCTCTATGTTGGCGGACATGAGCGGATG 282
 Db 120 CATCCGATGGACGGAAAGCAGCGGGCTCTCTATGTTGGCGGACATGAGCGGATG 282
 QY 283 ATTCGATCCCTACAGCGAAAGGAGGAGCTGGAGCTATGGACAACTGCTAAATGCT 342
 Db 178 ATGGCCCTATAATGAGAAGGAGGAGCTGGAGCTGGAGCTGGAGCTGGTCA 293
 QY 343 AAGGTAAACGTTACTCCGGTCTGTGTCATGTTATGACCCGGTACTTTAG 398
 Db 238 AAGATTAACGGTCACTCCAGGGTCAGCTGGCCATTTATGAACTGGATGTTCA 293
 RESULT 14
 AV808550/c
 LOCUS AV808550 423 bp mRNA linear EST 29-MAR-2002
 DEFINITION AV808550 RAFL9 Arabidopsis thaliana cDNA clone RAFL9-55-E15 3',
 mRNA sequence.
 ACCESSION AV808550
 VERSION 1
 KEYWORD SOURCE EST,
 ORGANISM thale cress.
 REFERENCE
 AUTHORS Eukaryota; Viridiplanteae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 423)
 Saki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., M uramatsu, M., Hayashizaki, Y., and Shinozaki, K.
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Saki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai', Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rtc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XbaI was ligated to modified Lambda FIC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sall. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
 FEATURES source
 Location/Qualifiers 1. 423
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="RAFL09-55-E15"
 /clone_line="RAFL9"
 /dev_stage="plants at various developmental stages from germination to mature seeds"
 /lab_host="DH10B"
 /note="Site_1: BamHI; Site_2: Sall; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
 BASE COUNT 121 a 101 c 72 g 129 t
 ORIGIN
 Query Match 27.9%; Score 112.6; DB 10; Length 423;
 Best Local Similarity 64.2%; Pred. No. 2 8e-27;
 Matches 201; Conservative 0; Mismatches 109; Indels 3; Gaps 2;
 QY 92 CAGCTCCGACCGAGCGCTGCTCGTGTATGCTCGAGAACGGGTCACTCAAAGT 151
 Db 423 CATCTCCAACCCACATTGTTGATTCGGAATCTCCAAATCAAATGTCAGAGAT 364
 QY 152 TCATCGAGGTAACAGAGCGAACTCAAAGAACATGTCAGCTGGCATCTGGGGGGGTG 211
 Db 363 TTGTGAAACCAACAGCGAGGATGCGAGAGTCTACACGGAGCTGCTGGGGTGTG 305
 QY 212 AGAAACTCGCATCGATGCGGAAGAGCGGGGCTCTCTATGTTGGCCGACA 271
 Db 304 AAAGAGTTAGGGATCGAGTCAGCAAGAACGATGGGGT-TCTACTGTGGGCHATA 247
 QY 272 TCGAGGATGATTCGATCCATCGAGGAAAGGAGGAGCTGGAGCTATGGACAACCTGC 331
 Db 246 TGCAGGAGATGATTTCATCTACAGCGGAAGAGGAGATGGAGCTGGAGACAGCTC 187
 QY 332 TAAACATGCTAAGGAAACCTTACTCCGGTCTGTGTCATGTTATGACCCGGCT 391
 Db 186 TGACATTTGGCGAAGATCAATGTCATACCGGAGCTGTTGTCAGTACCGACCGGAT 127
 QY 392 ACTTTAGCCCTG 404
 Db 126 GGTTCCGATCTG 114
 RESULT 15
 AV820681/c
 LOCUS AV820681 420 bp mRNA linear EST 01-APR-2002
 DEFINITION AV820681 RAFL11 Arabidopsis thaliana cDNA clone RAFL11-11-L09 3',
 mRNA sequence.
 ACCESSION AV820681
 VERSION 1
 KEYWORD SOURCE EST,
 ORGANISM thale cress.
 REFERENCE
 AUTHORS Arabidopsis thaliana
 Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 420)
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., M uramatsu, M., Hayashizaki, Y., and Shinozaki, K.
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai', Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rtc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XbaI was ligated to modified Lambda FIC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sall. This clone is in a modified pBluescript vector. Please visit our web

site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES	Location/Qualifiers
source	1. 420
	/organism="Arabidopsis thaliana"
	/db_xref="Taxon:3702"
	/clone="RAFL1-11-L09"
	/clone.lib="RAFL1"
	/dev_stage="plants at various developmental stages from germination to mature seeds"
	/lab_host="DNI0B"
	/note="Site_1: BamHI; Site_2: Sall; subjected to various treatments (dehydration, cold, high salt, ABA, heat and UV). Dark-grown plants"
BASE COUNT	122 a 105 c 64 g 129 t
ORIGIN	

Query	Match	Score	DB	Length
Best	Local Similarity	70.5%	107.2	420
Matches	171; Conservative	70.7%	Pred. No. 2e-25	
			Mismatches	68;
			Indels	3;
			Gaps	2;
QY	163 AACAGGGAAACTCAAGAATGTTACCGTCATTCGAGGGGTGAAAGAACTCGG	222		
Db	408 AACGGCAGATGGTGCAGATTCATCGGGACTCGGG-AGGGGTGAAAGAGT	350		
QY	223 CATCGATGCCACGGAAAGGAGCGGGCTCTATGTTGGCCGACATGGGATG	282		
Db	349 GATCGAGTGCACAGAAGCAATGGGGT-TCTACTGTTGGCTGATATGGGGATG	292		
QY	283 ATTCGATCTACACCGAAAAGGAGGGCTCGACATGGACAGATGCTAAACATGCT	342		
Db	291 ATTCATCTTACACCGAAAAGGGAGATGAGGTGGACAGCTCTTGACATTGGC	232		
QY	343 AAGCTAACGTTACTCCGGTTTGTGTCATGTTATGAAACCCGGTACTTTAGCTC	402		
Db	231 AAGCTAACGTTACTCCGGTTTGTGTCATGTTATGAAACCCGGTACTTTAGCTC	172		
QY	403 TG 404			
Db	171 TG 170			

Search completed: March 11, 2003, 01:40:14
Job time : 1217 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 00:11:12 ; Search time 43 Seconds

(without alignments)
2881.335 Million cell updates/sec

Title: US-09-975-842-1

Perfect score: 404
Sequence: 1.99gtggccgggttcaggat.....cccggtacttttagctctg 404

Scoring table: IDENTITY_NUC
Gapext 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

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2: /cgn2_6/ptodata/lina/5B_COMB.seq: *
3: /cgn2_6/ptodata/lina/6A_COMB.seq: *
4: /cgn2_6/ptodata/lina/6B_COMB.seq: *
5: /cgn2_6/ptodata/lina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/lina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

1 194.8 48.2 1743 4 US-09-171-482-1 Sequence 1, Appli

2 98.4 24.4 4459 4 US-09-363-243-2 Sequence 2, Appli

3 98 24.3 1384 2 US-08-850-577-1 Sequence 1, Appli

4 86.6 20.9 961 4 US-08-846-268-1 Sequence 3, Appli

5 84.6 20.9 968 4 US-08-846-268-1 Sequence 1, Appli

6 83.8 20.7 994 2 US-08-850-577-7 Sequence 2, Appli

7 83.6 20.7 1878 1 US-08-874-194-3 Sequence 4, Appli

8 80.4 19.9 1196 3 US-09-043-627-7 Sequence 5, Appli

9 80.4 19.9 1113 3 US-09-043-627-9 Sequence 6, Appli

10 78.8 19.5 1712 2 US-08-632-598-1 Sequence 7, Appli

11 78.8 19.5 1712 4 US-09-231-240-1 Sequence 8, Appli

12 77 19.1 1080 3 US-09-043-627-1 Sequence 9, Appli

13 72.4 17.9 1945 1 US-08-774-194-1 Sequence 10, Appli

14 72.4 17.9 2040 2 US-08-995-412B-11 Sequence 11, Appli

15 72.4 17.9 2040 4 US-09-673-768-1 Sequence 12, Appli

16 72.4 17.9 2678 1 US-08-724-194-2 Sequence 13, Appli

17 67.6 16.7 1703 4 US-08-978-313-18 Sequence 14, Appli

18 64.4 15.9 1104 3 US-09-043-627-3 Sequence 15, Appli

19 64.4 15.9 2330 4 US-08-378-313-24 Sequence 16, Appli

20 64.4 15.9 7244 4 US-08-078-313-26 Sequence 17, Appli

21 62.8 15.5 13397 2 US-08-673-768-1 Sequence 18, Appli

22 62.8 15.5 15397 2 US-08-673-768-1 Sequence 19, Appli

23 61.6 15.2 5613 2 US-08-663-418-1 Sequence 20, Appli

24 61.2 15.1 1800 1 US-08-909-457A-8 Sequence 21, Appli

25 61.2 15.1 1800 1 US-08-553-943-8 Sequence 22, Appli

26 61.2 15.1 1800 5 PCT-US91-09437-8 Sequence 23, Appli

27 59.6 14.8 1888 1 US-08-485-107-1 Sequence 24, Appli

ALIGNMENTS

RESULT 1
US-09-171-482-1

; Sequence 1, Application US/09171482A

; Patent No. 6184449

; GENERAL INFORMATION:

; APPLICANT: Ranu, Rajinder S.

; TITLE OF INVENTION: A 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM

; FILE REFERENCE: TAGAWA - ROSE

; CURRENT APPLICATION NUMBER: US/09/171-482A

; CURRENT FILING DATE: 1998-10-19

; EARLIER APPLICATION NUMBER: PCT/US97/17644, Published 1998-April-09; 1996-Oct-01

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: Word Perfect 6.1

; SEQ ID NO: 1

; LENGTH: 1743

; TYPE: DNA

; ORGANISM: Rosa kardinal

US-09-171-482-1

Query Match 48.2%; Score 194.8; DB 4; Length 1743;

Best Local Similarity 71.2%; Pred: No 5.5e-59; DB Matches 285; Conservative 0; Mismatches 112; Indels 3; Gaps 2;

QY 5 TCGCGGGTTCTAGATGGGGTTATCTACTCTTACACAGGAGACGCTCTACTACTGCCA 64

Db 1232 TTCCAGGTTTCAAGGTGGGTGCATCTACTCTTACACAGAATGTTGCTGCTGCTA 1291

QY 65 AAAGTGTGACGATTTCATCCATTCTAGCTCGAGGAGGGCTGTCGTGTTATGC 124

Db 1292 AAAAGTGTGACGAGGTCTCTCTATCCTGGCCCATCTCAAGGTTCTTATCTGTG 1351

QY 125 TCTGGAGACGGGGTCACTCAAAGTTCATGGAGTAACAGAGGAAACCAAAGAA 184

Db 1352 TTTCAGACACCAATTATGCTAAAGTCTCCAGGATTAACAGAGAAGGGCTCGTGGAA 1411

QY 185 TGTACGCTGCACTGGCGGGGTGAGAACACTGGCATCGAGCACGAAACGAGC 244

Db 1412 TGTATCTTAGTTGTGAC-AGGATGAACTGGCATTTGGGCTACAGAAG 1470

QY 245 GGAGGCTCTCATTTGTTGGCCGACATGACGGATGATGATGTCATCAGGAAAG 304

Db 1471 GGGG - TTCTACTGTTGGCGAGCTTGAGGGTTAATTCGCTCTTACAGTGAAG 1528

QY 305 GAGAGCTGAGCTATGGGACAGTGCTAACTGGTAAACGGTACTCCGGTT 364

Db 1529 GGGAGCTGACTCTGGATAGTGTGAGTGTAGGTAACGTTACTCCCTGGAT 1588

RESULT 2
US-09-363-243-2
Sequence 2, Application US/09363243
Patent No. 6414221
GENERAL INFORMATION:
APPLICANT: Oetker, Juerg H.
APPLICANT: Shiu, Oi Yin
APPLICANT: Yang, Shang Fa
APPLICANT: Yip, Win Kin
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Transiently Activated Stress-Inducible Plant Promoters
FILE REFERENCE: 023070-097000US
CURRENT APPLICATION NUMBER: US/09/363,243
CURRENT FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4459
TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
OTHER INFORMATION: 1-aminocyclopropane-1-carboxylic acid (ACC)
NAME/KEY: exon
LOCATION: (2464)..(2742)
NAME/KEY: intron
LOCATION: (2743)..(2845)
NAME/KEY: exon
LOCATION: (2845)..(3006)
NAME/KEY: intron
LOCATION: (3007)..(3102)
NAME/KEY: exon
LOCATION: (3103)..(4066)
NAME/KEY: CDS
LOCATION: join(2464..2742, 2846..3006, 3103..4066),
US-09-363-243-2

Query Match 24.4%; Score 98; DB 4; Length 4459;
Best Local Similarity 56.3%; Pred. No. 1.2e-24; Mismatches 171; Indels 3; Gaps 2;
Matches 224; Conservative 0; Mismatches 171; Indels 3; Gaps 2;

QY 1 GGGTGCCGGGTTAGGATGGGTTATCTACCTCTAACGAGAACGGTCTCACT 60
Db 3485 GGACATTCAGGATTCAGTGGCATTATTCACAGACGAATAGGGTCGTCTCGA 3544
QY 61 GCCAAAGTGTAGAGATTCATCCATTCAAGCTTCAGCTCCGAGCAGCGCTGCTGTT 120
Db 3545 GCCACAAATGTCAGTTGTTGATTAATTCACTCAACTCATACCTCTTCCTCGCT 3604
QY 121 ATGCTCTCGACAGGGTTCACTCAAAGTTCATCGAGTAACAGACGAGACTCAA 180
Db 3605 TTGCTATCAGACAAAGTTCACGAAATTACGGTCTGAAATTCAAAAGAGGCTGAA 3664
QY 181 AGATGTACCTGATTCGGGGGTGAAACTCGCATCCGATGAGGAAAG 240
Db 3665 AAAGACATGAACTGAGATCTAGTGGTGTCTAAACAA-TTGAA-TAAGGTGAGAG 3723
QY 241 CAGCGAGGCTCTCTATGGTGGCCGACATGAGGATGATCGATCTAGCGAA 300
Db 3724 CAATCTGCTGTTGTTGATGAGACATCTTAAAGTCAACACATT 3781
QY 301 AAGAGAGAGTCGACATGGTCTAAGTCAAGTGTACTCC 360
Db 3782 GATGGAGAATGGAAATTGGAAATAGTGTAGCAAGTAGGCTAAATTTCAGCT 3841
QY 361 GGTCTGTGTCATGTGAAACCGGTACTTTAG 398
Db 3842 GGATGTCGACGCGTCACTGAGCAACGGGTTGGTTCG 3879
US-09-363-243-2

Query Match 24.3%; Score 98; DB 2; Length 1384;
Best Local Similarity 55.9%; Pred. No. 9.2e-25; Mismatches 175; Indels 3; Gaps 2;
Matches 226; Conservative 0; Mismatches 175; Indels 3; Gaps 2;

QY 1 GGGTGCCGGGTTAGGATGGGTTATCTACCTCTAACGAGAACGGTCTCACT 60
Db 970 GGTCTTCGCCGTTTCGAGTTGGGACCATTTACTGCTGACGATATGTGTGAGACA 1029
QY 61 GCCAAAGTGTAGAGATTCATCCATTCACTCAAGCTTCAGCTCCGAGCAGCGCTGCTGTT 120
Db 1030 GCGAGAGGAGTTCAGCTTCACCGCTTGTGTCAGACACACATGTTGGCTCC 1089
QY 121 ATGCTCTCGACACGGGTTCACTAACAGTCATCGAGGAAACGAGGAAACTCAA 180
Db 1090 ATGTTGTCAGTGAAGAGTTAACGGGTTAGGAGAACTACATAAGGATAAACCGTGAAGGCTTAGG 1149
QY 181 AGATGTACCGCTCGATTCGGGGGTGAAACTCGCATCCGAGCAGCGCTGCTGAA 240

RESULT 3
US-08-860-577-1
Sequence 1, Application US/08860577
Patent No. 5998702
GENERAL INFORMATION:
APPLICANT: Boesshore, Maury L.
APPLICANT: Deng, Rosaline Z.
APPLICANT: Caney, Kim J.
APPLICANT: Ruttencutter, Glen E.
APPLICANT: Reynolds, John F.
TITLE OF INVENTION: Transgenic Plants Expressing ACC
TITLE OF INVENTION: Synthase Genes
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milmanow & Katz, Ltd.
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite 4700
CITY: Chicago
STATE: IL
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatientIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,577
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V.
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1384 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 2..39
FEATURE:
NAME/KEY: CDS
LOCATION: 135..433
FEATURE:
NAME/KEY: CDS
LOCATION: 595..1383
US-08-860-577-1

Query Match 24.3%; Score 98; DB 2; Length 1384;
Best Local Similarity 55.9%; Pred. No. 9.2e-25; Mismatches 175; Indels 3; Gaps 2;
Matches 226; Conservative 0; Mismatches 175; Indels 3; Gaps 2;

QY 1 GGGTGCCGGGTTAGGATGGGTTATCTACCTCTAACGAGAACGGTCTCACT 60
Db 970 GGTCTTCGCCGTTTCGAGTTGGGACCATTTACTGCTGACGATATGTGTGAGACA 1029
QY 61 GCCAAAGTGTAGAGATTCATCCATTCACTCAAGCTTCAGCTCCGAGCAGCGCTGCTGTT 120
Db 1030 GCGAGAGGAGTTCAGCTTCACCGCTTGTGTCAGACACACATGTTGGCTCC 1089
QY 121 ATGCTCTCGACACGGGTTCACTAACAGTCATCGAGGAAACGAGGAAACTCAA 180
Db 1090 ATGTTGTCAGTGAAGAGTTAACGGGTTAGGAGAACTACATAAGGATAAACCGTGAAGGCTTAGG 1149
QY 181 AGATGTACCGCTCGATTCGGGGGTGAAACTCGCATCCGAGCAGCGCTGCTGAA 240

Matches 205; Conservative 0; Mismatches 159; Indels 3; Gaps 2;

Db 1150 AGAGGGTAGAGACAAATGIGGAGGGCTT-AAGAGGCAGGATCGAGTGTGTTGAAGGG 1208
 Qy 241 CAGGGAGCTCTCTATGTGGGCCACATGAGCGGATTGATTCGATCCPACAGCGA 300
 Db 1209 TAATGAGGTT-TGTCCTGTTGATGAATTGGTTCTTGCTGACGAAACGAA 1266
 Qy 301 AAAGGAGACTCGAGCTATGGGACAAGTGCTAACATGCTAAGGTAACGTTACGCC 360
 Db 1267 CAAGGCAGCTCGAGCTTGGGAGTGATCTGAAGGACTAAAGCTGATAATCTCCT 1326
 Qy 361 GGTTCTGTTGTCATTGATGTTAGGATGGTTAGGATTG 404
 Db 1327 GGATCTGTCGCAATTGCTCGGAGTATGGATGGTTAGGATTG 1370

RESULT 4
 US-08-846-826A-3
 ; Sequence 3, Application US/08846826A
 ; GENERAL INFORMATION:
 ; APPLICANT: Botella, Jose
 ; APPLICANT: Sanewski, Garth
 ; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
 ; STREET: One Commerce Square, 2005 Market Street, 22nd
 ; CITY: Floor
 ; STATE: Philadelphia
 ; COUNTRY: Pennsylvania
 ; ZIP: 19103-7086
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/846,826A
 ; FILING DATE: 01-MAY-1997
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: AU PN9582
 ; FILING DATE: 01-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Nadel Esq., Alan S.
 ; REGISTRATION NUMBER: 27,363
 ; REFERENCE/DOCKET NUMBER: 8/95-11
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-965-1280
 ; TELEFAX: 831-494
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 961 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..102
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: 103..124
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 195..951
 ; US-08-846-826A-3

Query Match 21.4%; Score 86.6; DB 4; Length 961;
 Best Local Similarity 55.9%; Pred. No. 8.4e-21;

RESULT 5
 US-08-846-826A-1
 ; Sequence 1, Application US/08846826A
 ; GENERAL INFORMATION:
 ; PATENT NO. 619639
 ; APPLICANT: Botella, Jose
 ; APPLICANT: Sanewski, Garth
 ; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
 ; STREET: One Commerce Square, 2005 Market Street, 22nd
 ; CITY: Floor
 ; STATE: Philadelphia
 ; COUNTRY: Pennsylvania
 ; ZIP: 19103-7086
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/846,826A
 ; FILING DATE: 01-MAY-1997
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: AU PN9582
 ; FILING DATE: 01-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Nadel Esq., Alan S.
 ; REGISTRATION NUMBER: 27,363
 ; REFERENCE/DOCKET NUMBER: 8/95-11
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-965-1280
 ; TELEFAX: 831-494
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 968 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double

Qy 1 GGATTCGCGGGTCAGGATGGCGTTATCTACCTCTACAGAGAACGCTCACT 60
 Db 567 GGCTTACAGGCTTCTGGCTGGCGTCAACATCCAAATAGGGTGGTCTCCACG 626
 Qy 61 GCGAAAGTGAAGATTTCATCCATTCTACGCTCCAGCAGCGCTGCTGCGT 120
 Db 627 GCGACCAAGTGTGAGCTTGGCTCATCTCCCTCAACTCAGTACTCTGCTCCTG 686
 Qy 121 ATGCTCTCGACACGGGTCACAAAGTCATCGAGGTAACAGAGGAAACTCAA 180
 Db 687 TTGCTCTCGACAGGAGTACAGCGAACTACATAGCGAGACAAGAGCGACT-TAG 745
 Qy 181 AGATGTCGTCGTCATTGGGGGGTTGAAGAACATGGATCCATGACCGAAG 240
 Db 746 AGACGGCAAAAGGGCTCACCGAGACTACATAGCGAGACAAGAGCGCT-TAG 805
 Qy 241 CAGGGAGCTCTCTATGTGGGCCACATGAGCGGATTGATTCGATCCCTACAGCGA 300
 Db 806 CAATGCGAGCTT-GTGTGTTGTCGACATGGCACTTAAGCTAACGTTACGCC 360
 Qy 301 AAAGGAGACTCGAGCTATGGGACAAGTGCTAACATGCTAAGGTAACAGT 923
 Db 864 GAAGGAGAGTGGAGCTGGAAAGGATAGTCATGATGTTGGGACTAAACATTTCCG 923
 Qy 361 GGTTCTT 367
 Db 924 GGCTCTT 930

FILING DATE: 01-OCT-1996
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: SANTANGELO, LUKE
 REGISTRATION NUMBER: 31..997
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (970) 224-3100
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1878 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-724-194-3

Query Match 20.7%; Score 83.6; DB 1; Length 1878;
 Best Local Similarity 53.7%; Pred. No. 1..4e-19;
 Matches 217; Conservative 0; Mismatches 184; Indels 3; Gaps 2;
 QY 1 GGGTCCCGGGTTCAAGATGGCGTTATCTACTCCATACACAGGAACTGGCTCAGCTCGAGGAACTCGACCTAATGCA
 Db 953 GGCTTCCCTGGCTCAGGGGGATGTCCTACACTCTACATGAGCCAGTGGAAATGT 1012

QY 61 GCCAAAGAAGTGGACGGAGATTTCATCCATTTCAGCTCGACCCAGGCCCTGGCTGCGCT
 Db 1013 GCGGAAAGATGTCAGTTCGCGCTGTATCCACAACTCGACCTAATGCA 1072

QY 121 ATGCCTCGGACGGGGTCACTCAAAGTCTACGGAGAACAGAGCAACTGAA 180
 Db 1073 ATGCCTCGGACGGATGATGGCTGGCGGACATGGGGATGATTCATCCCTACAGGAA 1132

QY 181 AGAACTGAGCTGCAATGCTGGAGAACACTGGCATCCGATGAGGGAA 240
 Db 1133 AGAAAGTACACACTCTACAAGAGGGCTGCA-CAGTGAACATGATGGCTAAAGAG 1191

QY 241 CAGCGAGGCTCTCATGGGGGAGATGATTCATCCCTACAGGAA 300
 Db 1192 CAATGGGGGTTATCAT-ATGGATGACTGGAGGCTCTCAAGGAGAACACT 1249

QY 301 AAAGGAGAGCTGAGCTATGGGACAGTGTCAACATGCTAAGGTAACGTACTCC 360
 Db 1250 GAGGGGAGATGGCTGTGATGTATGAAACCGGGTCACTTAGCCCTCTG 404

QY 361 GGTTCTGTGTCATGTATGAACTGGAGAGGATAATCAAGAGTCAGCA 1309
 Db 1310 GGGGGCTGTCATGTCTCGGAGCCAGGGTGTAGAGCTG 1353

RESULT 8
 US-09-043-627-7
 ; Sequence 7, Application US/09043627
 ; Patent No. 6124525
 ; GENERAL INFORMATION:
 ; APPLICANT: Botella, Jose Ramon
 ; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
 ; STREET: 100 Thonet Circle, Suite 306
 ; CITY: Princeton
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08540-5662
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/043,627
 ; FILING DATE: 20-MAR-1998
 ; CLASSIFICATION: 800

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU96/00591
 FILING DATE: 20-SEP-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: AU PN5559
 FILING DATE: 20-SEP-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: AU PN9603
 FILING DATE: 02-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Bernstein, Scott N.
 REGISTRATION NUMBER: 38..827
 REFERENCE/DOCKET NUMBER: 3573-11US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-924-8555
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 LENGTH: 1096 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1095
 ; US-09-043-627-7

Query Match 19.9%; Score 80.4; DB 3; Length 1096;
 Best Local Similarity 53.2%; Pred. No. 1..4e-18;
 Matches 215; Conservative 0; Mismatches 186; Indels 3; Gaps 2;
 QY 1 GGGTCCCGGGTTCAAGATGGCGTTATCTACTCCATACACAGGAACTCGACCTAATGCA
 Db 688 GGCTTCCCTGGCTTATGGGTAGGCTATGCTTATATTCTATATGTCAGTGTGAGTGT 747

QY 61 GCCAAAGAAGTGGACGGAGATTTCATCCATTTCAGCTCGACCCAGGCCCTGGCTGCGCT 120
 Db 748 ATCCGCAAGGTCAGCTGGTTGTTGATTCCTACAACTCGACCTAATTCCTGCTTC 807

QY 121 ATGCCTCGGACGGGGTCACTCAAAGTCTACGGAGAACAGAGCAACTGAA 180
 Db 808 ATGCCTCGGACGGGGTCACTCAAAGTCTACGGAGAACAGAGCAACTGAA 867

QY 181 AGAACTGAGCTGCAATGCTGGAGAACACTGGCATCCGATGAGGGAA 240
 Db 868 AAAGGTACCATATTTCAACAAAGAGACTGTG-AGAAAGTGGGATRACTGCTGAAGGG 926

QY 241 CAGCGAGGCTCTCATGGGGGAGATGATTCATCCCTACAGGAA 300
 Db 927 AAATGGGG-TCTCTCGTCTGGGGATGATTCATCCCTACAGGAAACAGT 984

QY 301 AAAGGAGAGCTGAGCTATGGGACAGTGTCAACATGCTAAGGTAACGTACTCC 360
 Db 985 GATGCCGAATGAACTATGGGACAGTGTCAACATGCTAAGGTAACGTACTCC 1044

QY 361 GGTTCTGTGTCATGTATGAACTGGAGAGGATAATCAAGAGTCAGCA 404
 Db 1045 GGCTTCCCTTCATGCCAGGAGCTGGTGTGAGCTG 1088

RESULT 9
 US-09-043-627-9
 ; Sequence 9, Application US/09043627
 ; Patent No. 6124525
 ; GENERAL INFORMATION:
 ; APPLICANT: Botella, Jose Ramon
 ; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
 ; STREET: 100 Thonet Circle, Suite 306
 ; CITY: Princeton

STATE: NJ
 COUNTRY: USA
 ZIP: 08540-3662
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatientIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/043, 627
 FILING DATE: 20-MAR-1998
 CLASSIFICATION: 800
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU96/00591
 FILING DATE: 20-SEP-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: AU PNP5559
 FILING DATE: 20-SEP-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: AU PNP603
 FILING DATE: 02-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Bernstein, Scott N.
 REGISTRATION NUMBER: 38,827
 REFERENCE/DOCKET NUMBER: 3573-11US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-924-3036
 TELEFAX: 609-924-3555
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1113 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1113
 ; US-09-043-627-9

Query Match 19 9%; Score 80.4; DB 3; Length 1113;
 Best Local Similarity 53.2%; Pred. No. 1.4e-18;
 Matches 215; Conservative 0; Mismatches 186; Indels 3; Gaps 2;
 Qy 1 GGGTGGCCGGGTTCAGGATGGCGTTACCTACACTAACGAGAACCTGCTACTACT 60
 Db 694 GGGTTCAGGCTTGTAGGTCGGGATTATACATCATACAACTGATAGCTGGTGC 753
 Qy 61 GCCAAAAGTGAAGATTTCACTCACCTGAGCGAGCGCGCTGCTGCTGCTGCT 120
 Db 754 GCGTCGAAATGTCAGCTTGTGACTGTGATCACACATTAATGCTTC 813
 Qy 121 ATGGCTCGGACAGCGGTCACTCAAAGTCTACGAGTAACAGAGCAACTCAA 180
 Db 814 ATGGTATCAGATGATGAAATTGTGAGATAGTTGCTAAAGGCTTCGA 873
 Qy 181 AGAAATGAGCTGGATTCTGGCGGGGTGAAACAAACTCGGCATCCGAGCAAGGAAG 240
 Db 874 AAAGGCACAGGCTTC-ACATGGGGTATCTCAAGTAGGCTTGGTGTGAGAG 932
 Qy 241 CAGGGAGCTCTCTATGTTGGCGCATGAGCGGTATGATCGATCCTACAGCGA 300
 Db 933 CAATGCGGG--GCATTTCTGGATGGATTGGATCATCTCCAAAGGAGCAACTGAT 990
 Qy 301 AAAGGAGAGCTGAGCTATGGGAGAACAGTCTAACATGCTAAGGTTACTCC 360
 Db 991 GAACAGAGATAGACTGTGGAAGTGTAAATCAACAGAATTAATTAAATGTTCTCG 1050
 Qy 361 GGTCTGTGTCATGTATTGAAACCGGTACTTTAGCTCTG 404
 Db 1051 GGTCTTCCTCATGGCTTACAGGATGTTGGTTCGGTTG 1094

RESULT 10
 US-09-632-598-1
 Sequence 1, Application US/08632598
 ; Patient No. 588614
 ; GENERAL INFORMATION:
 ; APPLICANT: BIRD, COLIN R
 ; APPLICANT: FLETCHER, JONATHON D
 ; TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
 ; NUMBER OF SEQUENCES: 50
 ; CURRENT APPLICATION DATA:
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: CUSHMAN DARRY AND CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatientIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/632, 598
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 223355/SEES50112/US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 861-3000
 TELEFAX: 822-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1712 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: MUSA
 CLONE: ACS GENE
 ; US-08-632-598-1

Query Match 19 5%; Score 78.8; DB 2; Length 1712;
 Best Local Similarity 53.0%; Pred. No. 6.5e-18;
 Matches 214; Conservative 0; Mismatches 187; Indels 3; Gaps 2;
 Qy 1 GGGTGGCCGGGTCAAGGATGGGGTTATCTACTCTCTACACAGAGAACCTGCTACTACT 60
 Db 865 GGCGRCCCTGCCTCCGCGTGGGCTATATCTCTACACAGAGAACCTGCTACTACT 924
 Qy 61 GCCAAAAGTGAAGATTTCACTCACCTGAGCGAGCGCGCTGCTGCTGCTGCT 120
 Db 925 GCGAGGAAGTGTGCGAGCTTGGACTGGTCTCGCGACGAGCGACTCTGCTGCT 984
 Qy 121 ATGGCTCGGACAGCGGTCACTCAAAGTCTACGAGTAACAGAGCAACTCAA 180
 Db 985 ATGGTGGAGACGAGGAGTTCACCAAGAGTTCTCTAGCGAGCGCGAGGAGTGTGCT 1044
 Qy 181 AGAAATGAGCTGGATTCTGGCGGGGTGAAACAAACTCGGCATCCGAGCAAGGAAG 240
 Db 1045 GGGCGCGCAGGGTTTGGAGG-ACGGCGCAAGGAGTGGGAGTATGCTTGGCTG 1103
 Qy 241 CAGCGAGGAGTTCACCAAGAGTTCTCTAGCGAGCGCGAGTGAAGAACCTGCGATCCGAGTGGCAGCGA 300
 Db 1104 CAACGGGG--GCCTGTCCTGGATGGACTTGGCCGTTGCTGAAGGAGCGAGCGG 1161
 Qy 301 AAAGGAGAGCTGAGCTATGGGAGAACAGTCTAACATGCTAAGGTTACTCC 360
 Db 1162 GAGGGAGCTCCGGCTGTCGGGTGATCATCACAGACCTGAAAGCTCACATCTCGCC 1221

Db 1045 GGGCGCCGAGGGCTTTAGGG-ACGGCCCTAACGGAGTCGGGATTCATTGCTTGGACGG 1103
 Qy 361 GGTTCTGTTGTCATGTTATGGACCCGGCTACTTACCTCTG 404
 ; Sequence 1, Application US/09231240
 ; Patent No. 6263346
 ; GENERAL INFORMATION:
 ; APPLICANT: BIRD, COLIN R
 ; APPLICANT: FLETCHER, JONATHON D
 ; TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
 ; NUMBER OF SEQUENCES: 50
 ; ADDRESSEE: CUSHMAN DARBY AND CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/231,240
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/632,598
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N
 ; REFERENCE/DOCKET NUMBER: 16-773
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 861-3000
 ; TELEFAX: 822-0944
 ; TELEX: 6714627 CUSH
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1712 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: MUSA
 ; IMMEDIATE SOURCE:
 ; CLONE: ACS GENE
 ; US-09-231-240-1

Query Match 19.5%; Score 78.8; DB 4; Length 1712;
 Best Local Similarity 53.0%; Pred. No. 6.5e-18;
 Matches 214; Conservative 0; Mismatches 187; Indels 3; Gaps 2;

Qy 1 GGGTGGCGGGTTAGATGGGTTATCTACTCTAACAGAGAACGGTCACTACT 60
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Db 865 GGGCGCCGAGGGCTTTAGGG-ACGGCCCTAACGGAGTCGGGATTCATTGCTTGGACGG 1103
 Qy 61 GCCAAAGATGGAGATTTATCATTAGGTCGACGCCGGCTGCTCGAGGCAAGGCAAGCTCTCGTT 120
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Db 925 GCGAGGAGATGTCGAGCTTGGATGGCTCGTGCAGAGGCAAGCTCTCGTT 984
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Qy 121 ATGCTCTGGACACCGGTTACTCTAAAGTCATGGAGTAACAGAGGAACCTCAA 180
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Db 985 ATGCTGGAGACGGAGGTTACCAACGAGTTCTAGCGACGAGCGGACGAGGTGTCG 1044
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Qy 181 AGAAAGTACGCTGCCTTCGTTGGGGTTAGAGAACTCGGATCCGATCGATGCAAGGAAG 240
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Db 1104 CAAGCGGG--GCTGTTCTGGTGGACTTGGAGCCGTGCTGAAGGAAGCGGACGG 1161
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Qy 301 AAAGGAGACTCGAGCTATGGGACAACTGCTAACATGCTAGTAACAGTACTCC 360
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Db 1162 GAGCGGACGGCGGTTGGGGTACATCACAGACGTTGAAAGCTAACATCGCG 1221
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Qy 361 GGTTCTGTTGTCATGTTATGACCCGGCTACTTACCTCTG 404
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Db 1222 GGGCGCCGAGGGCTTTAGGG-ACGGCCCTAACGGAGTCGGGATTCATTGCTTGGACGG 1265
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

Qy 241 CAGCGGAGCTCTATGTTGGGCCACATGAGCGGATTTGATCTGATCTACAGCGA 300
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; NAME/KEY: CDS
 ; FEATURE: CDS
 ; LOCATION: 1..1080

RESULT 13
US-08-724-194-1
; Sequence 1, Application US/08724194
; Patent No. 5824875
; GENERAL INFORMATION:
; APPLICANT: RAMU, RAJINDER S.
; TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
; TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
; TITLE OF INVENTION: IN GERANIUMS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SANTANGELO LAW OFFICES PC
; STREET: 315 WEST OAK STREET, STE 701
; CITY: FORT COLLINS
; STATE: CO
; COUNTRY: USA
; ZIP: 80521
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,194
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SANTANGELO, LUKE
; REGISTRATION NUMBER: 31,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 224-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-724-194-1

Query Match 17.9%; Score 72.4; DB 1; Length 1945;
Best Local Similarity 53.7%; Pred. No. 1.3e-15;
Matches 217; Conservative 0; Mismatches 181; Indels 6; Gaps 3;

QY 1 GGGTGGCGGGTTCAGGATGGGGTATCTACTCTACAGGAGACGGCTCACT 750
Db 691 GGTCCTCCCGGATTCGAGTCGGATCGTGTATTCAGACGACACGGTGTAGTGGC 750
QY 61 GCCAAAGAATGAGAGATTCATCCATTCACTCAGCTGGCGCTGCGTCGT 120
Db 751 GCACGGAGATGCGAGCTCGGCTCGCTCGAGACAGACTGCGCC 810
QY 121 ATGCTCTCGGACAGCGGTCACTCAAAGTCTACAGGTAACAGCGAAACTCAA 180
Db 811 ATGCTATCCGGCGAGAAATTTCGCAAGATTACTGACTGAAGCGGAAGACTGCG 870
QY 181 AGATGTAGCTGCTGATTGTTGGGGGGTGAAGAAACTCGGATCCGATGGAAAG 240
Db 871 GAGGCCAGGATCTTCCTCTCCGGCTTGAGGAG-TGACATCCGCTGCTGGACG 929
QY 241 CAGGGAGGCTCTCTATGTTGGCCGACATGGCGGATGATCGATCTACAGCGA 300
Db 930 CAATGCCGGG--TCTTCGCTGCTGATGGACCTAGGGACCTCCCTCAAGAACGCCACCGA 987
QY 301 AAAGGAGAGCTGAGCTATGGAGAAGTGTCTAACATGCTAAAGTTACTCCC 360
Db 988 GACGGCAGACTCGAGCTGGCGGTAGTGAACATGTCAGCTCATGTCCTCC 1047
QY 361 GGTCCTGTTGTCATGTGTTGAACCGGGTACTTGTAGCTCTG 404
Db 1048 GGTCGTCGTTAATGCCGAGCAGGT 1078

RESULT 14
US-08-695-412B-11
; Sequence 11, Application US/08695412B
; Patent No. 5874269
; GENERAL INFORMATION:
; APPLICANT: STILES, JOHN I.
; APPLICANT: MOISYAD, STEFAN
; APPLICANT: NEUFANE, KABIR R.
; TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT
; TITLE OF INVENTION: DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE
; TITLE OF INVENTION: RIPENING OF COFFEE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JONES, DAY & POGUE
; STREET: NORTH POINT, 901 LAKESIDE AVENUE
; CITY: CLEVELAND
; STATE: OHIO
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS v. 5.1
; SOFTWARE: WordPerfect v. 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,412B
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,107
; ATTORNEY/AGENT INFORMATION:
; NAME: GRIFFITH, CALVIN P.
; REGISTRATION NUMBER: 34,831
; FILING DATE: 07-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 586-7050
; TELEFAX: (216) 579-0212
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2040 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

;

FEATURE:
NAME/KEY: CDS
LOCATION: 178..1653

Query Match 17.9%; Score 72.4; DB 2; Length 2040;
Best Local Similarity 52.0%; Pred. No. 1.3e-15; Mismatches 0; Indels 3; Gaps 2;
Matches 210; Conservative 0; Mismatches 191; Indels 3; Gaps 2;

Qy 1 GGGTTGGGGGTTCAAGATGGGGTTATCTACTCCATACAGGAACTGGCTCAGACT 60
Db 1027 GCCTTCCTGGATTCAAGATGGCTGCACTTGTGTTCAACACAAACCTCGCATCTGATGTCAGTGT 1086

Qy 61 GCCAAAAAGTGCAGGAGATTTCATCCATTCTACAGCTCCGACGCCAGCCTTGCTCGCGTT 120
Db 1087 GCTAGAAAAATGTCGAGTTTCGGCTCTGTTCAACACAAACCTCGCATCTGATGTCAGTGT 1146

Qy 121 ATGCCCTCGGACAGCGGTTACTCAAAGATTCATCGAGGAAACAGAGCAAACCTCAA 180
Db 1147 ATGTTACGGACAGAACGTTATGGACAAATCATTCCAGAGCTCAGAGAGATTAGCT 1206

Qy 181 AGAATGTCAGGCTCAATGCGATGTTGGGGGGTGGAGAACTGGCTCAGATGCTCAGTAGTGGCATGGCACCTTAAAG 1265
Db 1207 GCAAGGGATGGTCTTTCACAAAGAGGACTGTG-CTCAAGTAGTGGCATGGCACCTTAAAG 1265

Qy 241 CAGGGAGGCTCTCATTTGTTGGCCGACATGACGGGATGATGATGATCTACGGAA 300
Db 1266 CAGTCGGGC-CTTATTTCGGATGACTTAAGGAGACTCTCTAGGGAGTCACATT 1323

Qy 301 AAAGGAGAGCTGAGCTATGGACAACTTGCTAAACATGGTAAAGGTAAGGTAAAGTACTCC 360
Db 1324 GAGGAGAAATGGACACTTGAGGATCATATACTAGAAGTCAGTCAGTCAATGTTACCA 1383

Qy 361 GGTCTCTGTGTCATGTTGACCCGGCTACTTGCTAGCTG 404
Db 1384 GCCTATCTTCATTCAGAACCCAGGATGGTCAAGTGT 1427

RESULT 15

US-09-255-154D-11

Sequence 11, Application US/09255154D

Patent No. 6148474

GENERAL INFORMATION:

APPLICANT: STILES, JOHN T.
MOISYADI, ISTEFO
NEUPANE, KABI R.

TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT
DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE
RIPENING OF COFFEE

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: JONES, DAY, REAVIS & POGUE
STREET: NORTH POINT, 901 LAKESIDE AVENUE
CITY: CLEVELAND
STATE: OHIO
ZIP: 44114

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS v. 5.1

SOFTWARE: WordPerfect v. 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/255,154D
FILING DATE: 22-Feb-1999
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/695,412
FILING DATE: 12-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: GRIFFITH, CALVIN P.
REGISTRATION NUMBER: 34,831

;

REFERENCE/DOCKET NUMBER: 265036600002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (216) 586-7050
TELEFAX: (216) 579-0212

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 2040 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:
NAME/KEY: CDS
LOCATION: 178..1653
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Query Match 17.9%; Score 72.4; DB 4; Length 2040;
Best Local Similarity 52.0%; Pred. No. 1.3e-15; Mismatches 0; Indels 3; Gaps 2;
Matches 210; Conservative 0; Mismatches 191; Indels 3; Gaps 2;

Qy 1 GGGTTGGGGGTTCAAGATGGGGTTATCTACTCCATACAGGAACTGGCTCAGACT 60
Db 1027 GCTAGAAAAATGTCGAGTTTCGGCTCTGTTCAACACAAACCTCGCATCTGATGTCAGTGT 1086

Qy 61 GCCAAAAAGTGCAGGAGATTTCATCCATTCTACAGCTCCGACGCCAGCCTTGCTCGCGTT 120
Db 1087 GCTAGAAAAATGTCGAGTTTCGGCTCTGTTCAACACAAACCTCGCATCTGATGTCAGTGT 1146

Qy 121 ATGCCCTCGGACAGCGGTTACTCAAAGATTCATCGAGGAAACAGAGCAAACCTCAA 180
Db 1147 ATGTTACGGACAGAACGTTATGGACAAATCATTCCAGAGCTCAGAGAGATTAGCT 1206

Qy 181 AGAATGTCAGGCTCAATGCGATGTTGGGGGGTGGAGAACTGGCTCAGATGCTCAGTAGTGGCATGGCACCTTAAAG 1265
Db 1207 GCAAGGGATGGTCTTTCACAAAGAGGACTGTG-CTCAAGTAGTGGCATGGCACCTTAAAG 1265

Qy 241 CAGGGAGGCTCTCATTTGTTGGCCGACATGACGGGATGATGATGATCTACGGAA 300
Db 1266 CAGTCGGGC-CTTATTTCGGATGACTTAAGGAGACTCTCTAGGGAGTCACATT 1323

Qy 301 AAAGGAGAGCTGAGCTATGGACAACTTGCTAAACATGGTAAAGGTAAGGTAAAGTACTCC 360
Db 1324 GAGGAGAAATGGACACTTGAGGATCATATACTAGAAGTCAGTCAGTCAATGTTACCA 1383

Qy 361 GGTCTCTGTGTCATGTTGACCCGGCTACTTGCTAGCTG 404
Db 1384 GCCTATCTTCATTCAGAACCCAGGATGGTCAAGTGT 1427

Search completed: March 11, 2003, 01:19:55
Job time : 48 secs



OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 00:52:12 ; search time 61 Seconds (without alignments)

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 478924 seqs, 33959956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

1: /cgn2_6/podata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/podata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/podata/2/pubpna/US05_NEW_PUB.seq:*

4: /cgn2_6/podata/2/pubpna/US05_PUBCOMB.seq:*

5: /cgn2_6/podata/2/pubpna/US05_NEW_PUB.seq:*

6: /cgn2_6/podata/2/pubpna/PICTUS_PUBCOMB.seq:*

7: /cgn2_6/podata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/podata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/podata/2/pubpna/US09_NEW_PUB.seq:*

10: /cgn2_6/podata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/podata/2/pubpna/US10_NEW_PUB.seq:*

12: /cgn2_6/podata/2/pubpna/US10_PUBCOMB.seq:*

13: /cgn2_6/podata/2/pubpna/US50_NEW_PUB.seq:*

14: /cgn2_6/podata/2/pubpna/US50_PUBCOMB.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	194.8	48.2	1743	10	US-09-776-529A-1	Sequence 1, Appli
2	107.6	26.6	748	10	US-09-770-149-16	Sequence 16, Appli
3	107.6	26.6	1344	9	US-09-938-842A-1571	Sequence 1571, Ap
4	53.6	13.3	1488	9	US-09-938-842A-1726	Sequence 1726, Ap
5	31.6	7.8	46819	9	US-10-114-170-72	Sequence 72, Appli
6	30.4	7.5	1416	9	US-09-938-842A-593	Sequence 583, Appli
7	30.2	7.5	1416	9	US-09-938-842A-1711	Sequence 1711, Ap
8	30.2	7.5	2302	12	US-10-039-528-1711	Sequence 1711, Ap
9	30.2	7.5	7960	10	US-09-764-869-3327	Sequence 2327, Ap
10	30.2	7.5	17239	10	US-09-764-869-3326	Sequence 2326, Ap
11	30	7.4	353	10	US-09-924-035A-68	Sequence 68, Appli
12	29.8	7.4	398	9	US-09-954-531-90	Sequence 90, Appli
13	29.8	7.4	398	9	US-09-954-531-291	Sequence 291, Appli
14	29.8	7.4	398	9	US-09-954-531-508	Sequence 508, Appli
15	29.8	7.4	398	10	US-09-962-436-152	Sequence 152, Appli
16	29.8	7.4	398	10	US-09-980-300A-211	Sequence 1211, Appli
17	29.8	7.4	1113	9	US-09-738-626-3191	Sequence 3191, Appli
18	29.8	7.4	330940	9	US-09-778-626-1	Sequence 1, Appli
19	29.4	7.3	13819	10	US-09-764-877-596	Sequence 2596, Appli

ALIGNMENTS

RESULT 1
US-09-776-529A-1

; Sequence 1, Application US/09776529A
; Patent No. US20020083484A1

; GENERAL INFORMATION:
; APPLICANT: Tagawa Greenhouses, Inc.
; APPLICANT: Ranu, Rajinder S.
; TITLE OF INVENTION: A 1-Aminocyclopropane-1-Carboxylate Synthase Gene From Rosa
; TITLE OF INVENTION: Ethylene Levels In Roses
; FILE REFERENCE: Tagawa Rose
; CURRENT APPLICATION NUMBER: US/09/776,529A
; CURRENT FILING DATE: 2001-02-02
; PRIORITY APPLICATION NUMBER: US 08/724,194
; PRIORITY FILING DATE: 1996-10-01
; PRIORITY APPLICATION NUMBER: US 09/171,482
; PRIORITY FILING DATE: 1998-10-19
; PRIORITY APPLICATION NUMBER: PCT/US97/17644
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 1
; LENGTH: 1743

TYPE: DNA
; ORGANISM: Rosa kerdinal

Query Match 48.2%; Score 194.8; DB 10; Length 1743;
Best Local Similarity 71.2%; Pred: No 2.5e-57;
Matches 285; Conservative 0; Mismatches 112; Indels 3; Gaps 2;

QY	5	TGCCGGGTTCAGGATGGGGTTATCCTACTCCACAGGAGAGGTGCTCACTACTGCCA	64
QY	5	TGCCGGGTTCAGGATGGGGTTATCCTACTCCACAGGAGAGGTGCTCACTACTGCCA	64
Db	1232	TTCAGTTTCAGGTTGGTGGTGCCTTAACAGAAGTCTGACTGCTCA	1291
QY	65	AAAGTGTGAGGATTTCATCCATTGAGCTGAGCAGCAGCCTGCGTGTGCTATG	124
Db	1292	AAAGTGTGAGGATTTCATCCATTGAGCTGAGCAGCAGCCTGCGTGTGCTATG	1351
QY	125	TCTCGACACGGGGTCACTCAAGTTCATCGAGGTAACAGAGCGAACTCAAAAGAA	184
Db	1352	TTTAGACACCAATTATGCTTAAGTTCATCGAGGATTAACAGAGAAAGGCTCCGGAA	1411

RESULT 2
US-09-770-149-16/c
Sequence 16, Application US/09770149
; Sequence 16, Application US/09770149
; GENERAL INFORMATION:
; Patent No. US20020059663A1
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yiu, Yung
; APPLICANT: Nameka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Hoffman, Neil
; APPLICANT: Horban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178, 506
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 748
; TYPE: DNA
; FEATURE: NAME/KEY: misc_feature
; LOCATION: (1..:748)
; OTHER INFORMATION: n = A,T,C or G
; US-09-770-149-16

Query Match 26 6%; Score 107 6; DB 9; Length 1344;
Best Local Similarity 57 4%; Pred. No. 4.2e-27; Mismatches 169; Indels 3; Gaps 2;
Matches 232; Conservative 0; Mismatches 169; Indels 3; Gaps 2;

QY 1 GGGTGGCGGGTTCAGATGGCGTTATCACTCCACAAAGAGAACGTGCTCACTACT 60
Db 862 GGTCCTCCGGTTCGGCGGGAACTATACTCGTACACGATAATGTTGGAC 921
QY 61 GCCAAAGAGTGGAGATTCATCCACGGTTCAGCTTCGTCAGAC 120
Db 922 GCGAGAAGAGTGGAGCTTCAGCTTCAGCTTCAGACACATATGCTGGCTCT 981
QY 121 ATGCCTCGACACGGGTTCACTCAAAGTTCATCGAGGTAACAGAGGAACTCAA 180
Db 982 ATGTTGTCGATGAGGAGTTACGGAGAAGTCACTTAGGATAACACGGAAAGACTTGA 1041
QY 181 AGAATCTACGCTGATTCGTTGGCGGGGTGAAGAACCTGGCATCCGATGCGAA 240
Db 1042 AGACGGTAGATACCACTGTTGGAGGGCTT-AGAAGGGGGATGAGTGTGTCAGAAGG 1100
QY 241 CASGGAGSCTTCCTCTATGTTGGCGCGCATGGCGGAATGATGCGATCCGAGA 300
Db 1101 GAACCGCAGG-GCTATTGTTGGATGAATTGGTTCTGCTGCAAAAGAAACTAAA 1158
QY 301 AAAGGAGACTCGACATGGGACAGTCTAACATCTAACATGAACTAACGTTACTCCC 360
Db 260 GGATCTCGGCACTGCTGGAGCTGGATGGTTAGGGTTAGGGTT 217

RESULT 3
US-09-938-842A-1571
; Sequence 1571, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, JoeL
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: SPRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1571
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1571

Query Match 26 6%; Score 107 6; DB 9; Length 1344;
Best Local Similarity 57 4%; Pred. No. 4.2e-27; Mismatches 169; Indels 3; Gaps 2;
Matches 232; Conservative 0; Mismatches 169; Indels 3; Gaps 2;

QY 1 GGGTGGCGGGTTCAGATGGCGTTATCACTCCACAAAGAGAACGTGCTCACTACT 60
Db 862 GGTCCTCCGGTTCGGCGGGAACTATACTCGTACACGATAATGTTGGAC 921
QY 61 GCCAAAGAGTGGAGATTCATCCACGGTTCAGCTTCGTCAGAC 120
Db 922 GCGAGAAGAGTGGAGCTTCAGCTTCAGCTTCAGACACATATGCTGGCTCT 981
QY 121 ATGCCTCGACACGGGTTCACTCAAAGTTCATCGAGGTAACAGAGGAACTCAA 180
Db 982 ATGTTGTCGATGAGGAGTTACGGAGAAGTCACTTAGGATAACACGGAAAGACTTGA 1041
QY 181 AGAATCTACGCTGATTCGTTGGCGGGGTGAAGAACCTGGCATCCGATGCGAA 240
Db 1042 AGACGGTAGATACCACTGTTGGAGGGCTT-AGAAGGGGGATGAGTGTGTCAGAAGG 1100
QY 241 CASGGAGSCTTCCTCTATGTTGGCGCGCATGGCGGAATGATGCGATCCGAGA 300
Db 1101 GAACCGCAGG-GCTATTGTTGGATGAATTGGTTCTGCTGCAAAAGAAACTAAA 1158
QY 301 AAAGGAGACTCGACATGGGACAGTCTAACATCTAACATGAACTAACGTTACTCCC 360

RESULT 4

US-09-938-842A-1726

; Sequence 1726, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING FILE REFERENCE: SCRIP1300-3

; CURRENT FILING DATE: 2001-08-24

; PRIORITY FILING DATE: 2000-08-24

; PRIORITY APPLICATION NUMBER: US 60/264,647

PRIORITY FILING DATE: 2001-01-16

PRIORITY APPLICATION NUMBER: US 60/300,111

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1726

LENGTH: 1488

TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; US-09-938-842A-1726

Query Match 13.3%; Score 53.6; DB 9; Length 1488; Best Local Similarity 47.5%; Pred. No. 2.5e-08; Matches 192; Conservative 0; Mismatches 209; Indels 3; Gaps 1;

Qy 1 GGGTGGGGGTTAGATGGGGTATRACTCTACACGAAACGAGTC 60

Db 847 GGTCATGCTGGTTAGAGTTAGTATGATCTTACATGACAGGGTTCAGTC 906

Qy 61 GCGCAAAAGTGTACGAAATTCTACCAATTCTACGTCGACGGCTCTGGCGTAA 966

Db 907 GCGAAAGAAATGTCGAGTTGGCTCTGTTGTCACAAACCGACATTGATCGCTAA 966

Qy 121 ATGCTCGGGACACGGGTTACTCAAAGTCTACGGAGAACAGAGCGAAACTCAA 180

Db 967 ATGTATTCGATGAGAGTTGTTAGGAGGTTATCCGGAGAGCAATTGGGTAGCT 1026

Qy 181 AGAAATGACGCTGCACTGCTGGGGGTGAGAACTCGGCATCCGATGACGGAA 240

Db 1027 GCAAGGACCGCTGAGATAACCAACCGTTAGTGTATGGATGGTGGTT - AAAG 1083

Qy 241 CAGGGGAGGCTCTCATGTTGGCCGACATGAGGGATGATCGATCCAGCGAA 300

Db 1084 GCCAAGGCGGTTGTTGCTGGATGATTAAGAAATCTTGGAGACAGCACTT 1143

Qy 301 AAAGAGAGCTGAGCTATGGACAAAGTTGCTAAATGTTAAAGTTACTCCC 360

Db 1144 GATTGCGAACCGAACATATGGGTGATGTTCAACAAAGTGAACGCTCAACGGTCTCA 1203

Qy 361 GGTTCTGTGTCATGTTGAAACCGGCTACTTGTGCTG 404

Db 1204 GGCGGTCGTTCCATGCGAACCGGGATGGTTAGAGTATG 1247

RESULT 5

US-10-114-170-72/C

; Sequence 72, Application US/10114170

; Publication No. US20030023075A1

; GENERAL INFORMATION:

; APPLICANT: Blattner, Frederick R.

Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod

TITLE OF INVENTION: No. US20030023075A1 Sequences of E. coli 0157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quatles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,170

FILING DATE: 01-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/453,702

FILING DATE: 03-DEC-1999

APPLICATION NUMBER: 60/710,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Sevy, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 72:

SEQUENCE CHARACTERISTICS:

SEQUENCE DESCRIPTION: SEQ ID NO: 72:

LENGTH: 46819

TYPE: nucleic acid

STRAND EDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 72:

US-10-114-170-72

Query Match 7.8%; Score 31.6; DB 9; Length 46819; Best Local Similarity 50.7%; Pred. No. 6.4%; Matches 76; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 198 CGTGGCGGGGTGAGAACACGTCGGCATCCGATGACGGAGGCCTCTA 257

Db 37493 CATCGTGGCGCAGGTTAATTCGCTGAGAACATGCGATCAGCAAAGCTCTGAGCTGGTGT 37434

Qy 258 TTGTGGCCGACATGACGGATGATGTCGATCTACAGCGAAAGGAGGACCTCGAGCT 317

Db 37433 AAAGGCGCCAACATAGTGGCGTAATTAAAACGATCACAAGGAGCATCAGANGCA 37374

Qy 318 ATGGGAGAAGTGTGCTAACATGCTAAGGT 347

Db 37373 GGAAAGAAGTGGTCAGAACGCCATGT 37344

RESULT 6

US-09-938-842A-583

; Sequence 583, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING FILE REFERENCE: SCRIP1300-3

; TITLE OF INVENTION: SAME, AND METHODS OF USE

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; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO: 583
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-583

Query Match 7.5%; Score 30.4; DB 9; Length 1416;
Best Local Similarity 57.3%; Pred. No. 2.8; Mismatches 41; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 300 AAAGGGAGAGCTGAGCTATGGGCAAGTGTCTAACATGCTAGGTAAACGTTACTCC 359
Db 306 AAAACCGTCTCATGCTGGGACCGAGCTGATTAACAGAGTCGAGTTATGCCATACAG 365
QY 360 CGGTCTTGTGTTGATGGTATGGACCCGGTACT 395
Db 366 AGGTTTCTCACCGTGATATAAACCTGACACTT 401

RESULT 7
US-09-920-300A-1711/c
Sequence 1711, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E
; APPLICANT: Meadher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Sechrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920, 300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1711
; LENGTH: 2302
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-920-300A-1711

Query Match 7.5%; Score 30.4; DB 9; Length 1416;
Best Local Similarity 57.3%; Pred. No. 2.8; Mismatches 41; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 300 AAAGGGAGAGCTGAGCTATGGGCAAGTGTCTAACATGCTAGGTAAACGTTACTCC 359
Db 306 AAAACCGTCTCATGCTGGGACCGAGCTGATTAACAGAGTCGAGTTATGCCATACAG 365
QY 360 CGGTCTTGTGTTGATGGTATGGACCCGGTACT 395
Db 366 AGGTTTCTCACCGTGATATAAACCTGACACTT 401

RESULT 8
US-10-033-528-1711/c
Sequence 1711, Application US/10033528
; Patent No. US20020136721A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.

RESULT 9
US-09-764-869-2327/c
Sequence 2327, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764, 869
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/764, 869
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO: 2327
; LENGTH: 7960
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-869-2327

Query Match 7.5%; Score 30.2; DB 10; Length 2302;
Best Local Similarity 51.1%; Pred. No. 4.2; Mismatches 68; Indels 0; Gaps 0;
Matches 71; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 145 CAAAGTTCATCGGGTAACAGGGAAACTCAGAAAGATGTGGCTACATGGGG 204
Db 2129 CAAATAATAACAAATACACAGACGCTACATGAGAAAGCCATGTGGCTTACAGCT 2070
QY 205 GGGGTGAAGAACGGCATCCGATGTCAGGAAGAACCGGGCTTCCTATGTGG 264
Db 2069 GGGATGAGGACTCTGTCATGAGACATAGCACATGATTCTCCAGGGCAGA 2010
QY 265 GCGCACATGAGCGGATG 283
Db 2009 GAGGTGGCTGGAGATGA 1991

RESULT 10
US-09-764-869-2326/c
Sequence 2326, Application US/09764869
; Patent No. US20020061521A1
; APPLICANT: King, Gordon E.


```

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/7764,869
; CURRENT FILING DATE: 2001-01-17
; PRIORITY APPLICATION data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2326
; LENGTH: 17239
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-869-2326

Query Match 7.5%; Score 30.2; DB 10; Length 17239;
Best Local Similarity 51.1%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;
Matches 71; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 145 CAAAGTTCATCGAGTAAACAGACGAACTCAAAGAATGTTAGCTGTCATTCTGGGG 204
Db 17059 CAAATAATAACAAATACCAACAGAGACGCCATACATGAGAAAGCCATAGTGCCTCAAGCCT 17000

QY 205 GGGTGAAGAACTCGGCATCCGGTGGACGGAGGCTCTATGTGG 264
Db 16999 GGGATGAGACTCTAGTCCTAAATCTAGAAACATAGCACATGATTCCTCAGGCAGA 16940

QY 265 GCGCAGATGAGGGATGA 283
Db 16939 GAGGTGGCTGGAGATGA 16921

RESULT 11
US-09-924-035A-68
; Sequence 68, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
; APPLICANT: Grilach, Jrm
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924, 035A
; PRIORITY FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO: 68
; LENGTH: 353
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE: misc. feature
; LOCATION: (1)..(353)
; OTHER INFORMATION: n = A,T,C or G
; US-09-924-035A-68

RESULT 13
US-09-954-531-291
; Sequence 291, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Joe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 68929077
; CURRENT APPLICATION NUMBER: US/09/954, 531
; PRIORITY FILING DATE: 2002-05-02
; PRIORITY APPLICATION NUMBER: US/60/233, 133
; PRIORITY FILING DATE: 2000-09-18
; PRIORITY APPLICATION NUMBER: US/60/234, 009
; PRIORITY FILING DATE: 2000-09-20
; PRIORITY APPLICATION NUMBER: US/60/234, 034
; PRIORITY FILING DATE: 2000-09-20
; PRIORITY APPLICATION NUMBER: US/60/234, 509
; PRIORITY FILING DATE: 2000-09-22
; PRIORITY APPLICATION NUMBER: US/60/234, 567
; PRIORITY FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 291
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-954-531-291

Query Match 7.4%; Score 30; DB 10; Length 353;
Best Local Similarity 53.1%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 288 ATCCATACAGGAAAGAGAGCTGAGCTATGGGACAAGTGGCTAACATTGCTTAAGT 347
Db 135 ATCAGACAAAGCAAAACAAAGGACAAAGGAAATAGAGGAGCTGAAATCTAAGGTAGTC 194

QY 348 AAACGTTACTCCGGTCTGTGTCATGATGATGAGCCGGCTACTTGACCCGCC 400
Db 195 AATTTTATCCGGTCTCTCGATCTGAATGAAANNTCACTGTGTC 247

RESULT 12
US-09-954-531-90
; Sequence 90, Application US/09954531

Query Match 7.4%; Score 29.8; DB 9; Length 398;
Best Local Similarity 54.0%; Pred. No. 2.3; Mismatches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 145 CAAAGTTCATCGAGTAAACAGACGAACTCAAAGAATGTTAGCTGTCATTCTGGGG 204
Db 181 CAAATAATAACAAATACCAACAGAGACGCCATACATGAGAAAGCCATAGTGCCTCAAGCCT 257

QY 205 GGGTGAAGAACTCGGCATCCGGTGGACGGAGGCTCTATGTGG 264
Db 241 GGGGAGGAGACTCTAGTCCTAAATCTAGAAACATAGCACATGATTCCTCAGGCAGA 293

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RESULT 14
; Sequence 508 Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using cDNA
; FILE REFERENCE: 659290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 508
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-954-531-508

Query Match 7.4%; Score 29.8; DB 9; Length 398;
Best Local Similarity 54.0%; Pred. No. 2,3; Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 145 CAAAGCTTCAGGAGTAACAGAGGAAACCTAAAGAATGTCGCTTCAGGG 204
Db 181 CAAATATAACAAATACCAAGAGACCCATGAGAAAGCCATGCGCTTCAGCCT 240
QY 205 GGGTGTGAAACTCGGCATCCGCAAGCGGAGGGCTCTCA 257
Db 241 GGGATGAGGACTCTAGTCCTAAATCTTACACATGAGATCTCA 293

RESULT 15
US-09-962-436-152
; Sequence 152 Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 682290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 152
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-962-436-152

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Query Match 7.4%; Score 29.8; DB 10; Length 398;
Best Local Similarity 54.0%; Pred. No. 2,3; Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 145 CAAAGCTTCAGGAGTAACAGAGGAAACCTAAAGAATGTCGCTTCAGGG 204
Db 181 CAAATATAACAAATACCAAGAGACCCATGAGAAAGCCATGCGCTTCAGCCT 240
QY 205 GGGTGTGAAACTCGGCATCCGCAAGCGGAGGGCTCTCA 257
Db 241 GGGATGAGGACTCTAGTCCTAAATCTTACACATGAGATCTCA 293

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